```
                9          18          27          36          45          54
5'  GTG GGC ATG GTG GGC AAC GTC CTG CTG GTG CTG GTG ATC GCG CGG GTG CGC CGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg

               63          72          81          90          99         108
    CTG CAC AAC GTG ACG AAC TTC CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu

              117         126         135         144         153         162
    ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT GCC TTC GAG CCA CGC GGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly

              171         180         189         198         207         216
    TGG GTG TTC GGC GGC GGC CTG TGC CAC CTG GTC TTC TTC CTG CAG CCG GTC ACC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr

              225         234         243         252         261         270
    GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CGG TAC GTC GTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val

              279         288         297
    CTG GTG CAC CCG CTG AGG CGG CGC ATC 3'
    --- --- --- --- --- --- --- --- ---
    Leu Val His Pro Leu Arg Arg Arg Ile
```

FIG. 1

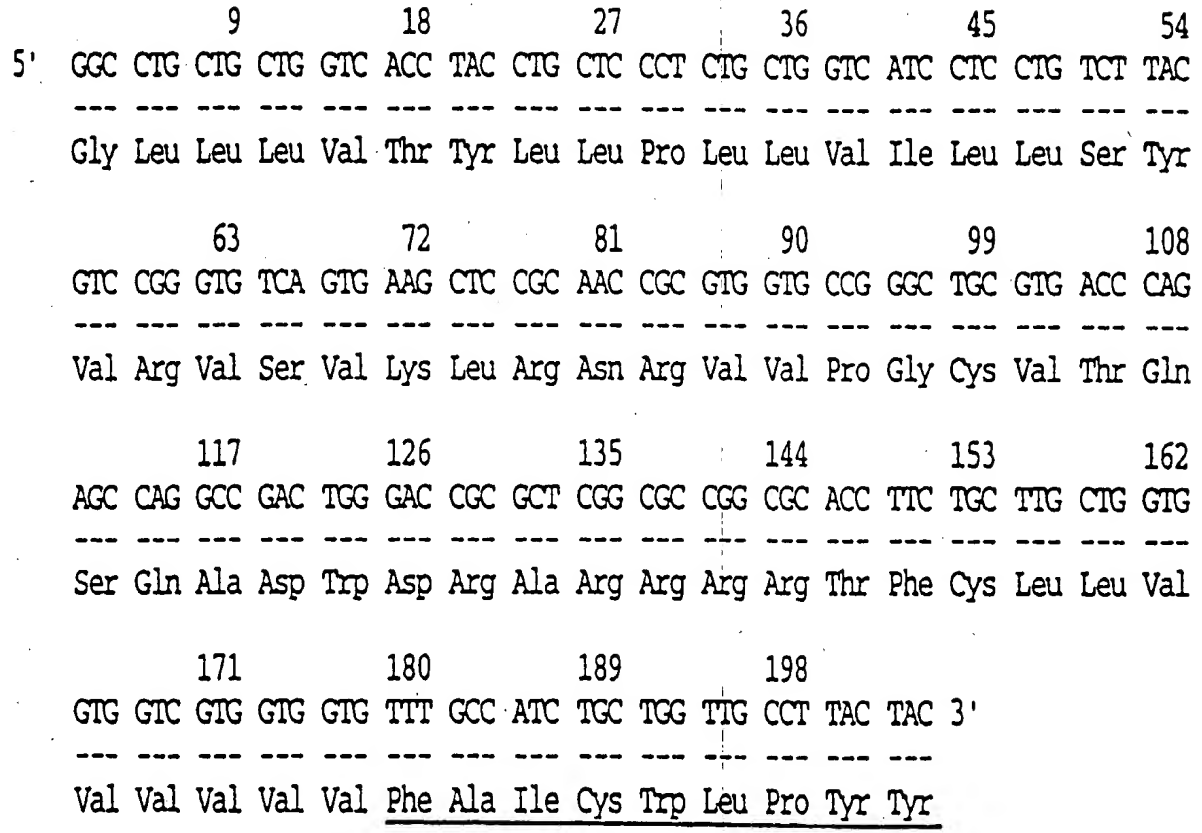

9 18 27 36 45 54
5' GGC CTG CTG CTG GTC ACC TAC CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC
Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr
63 72 81 90 99 108
GTC CGG GTG TCA GTG AAG CTC CGC AAC CGC GTG GTG CCG GGC TGC GTG ACC CAG
Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Cys Val Thr Gln
117 126 135 144 153 162
AGC CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG
Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val
171 180 189 198
GTG GTC GTG GTG GTG TTT GCC ATC TGC TGG TTG CCT TAC TAC 3'
Val Val Val Val Val Phe Ala Ile Cys Trp Leu Pro Tyr Tyr

FIG. 2

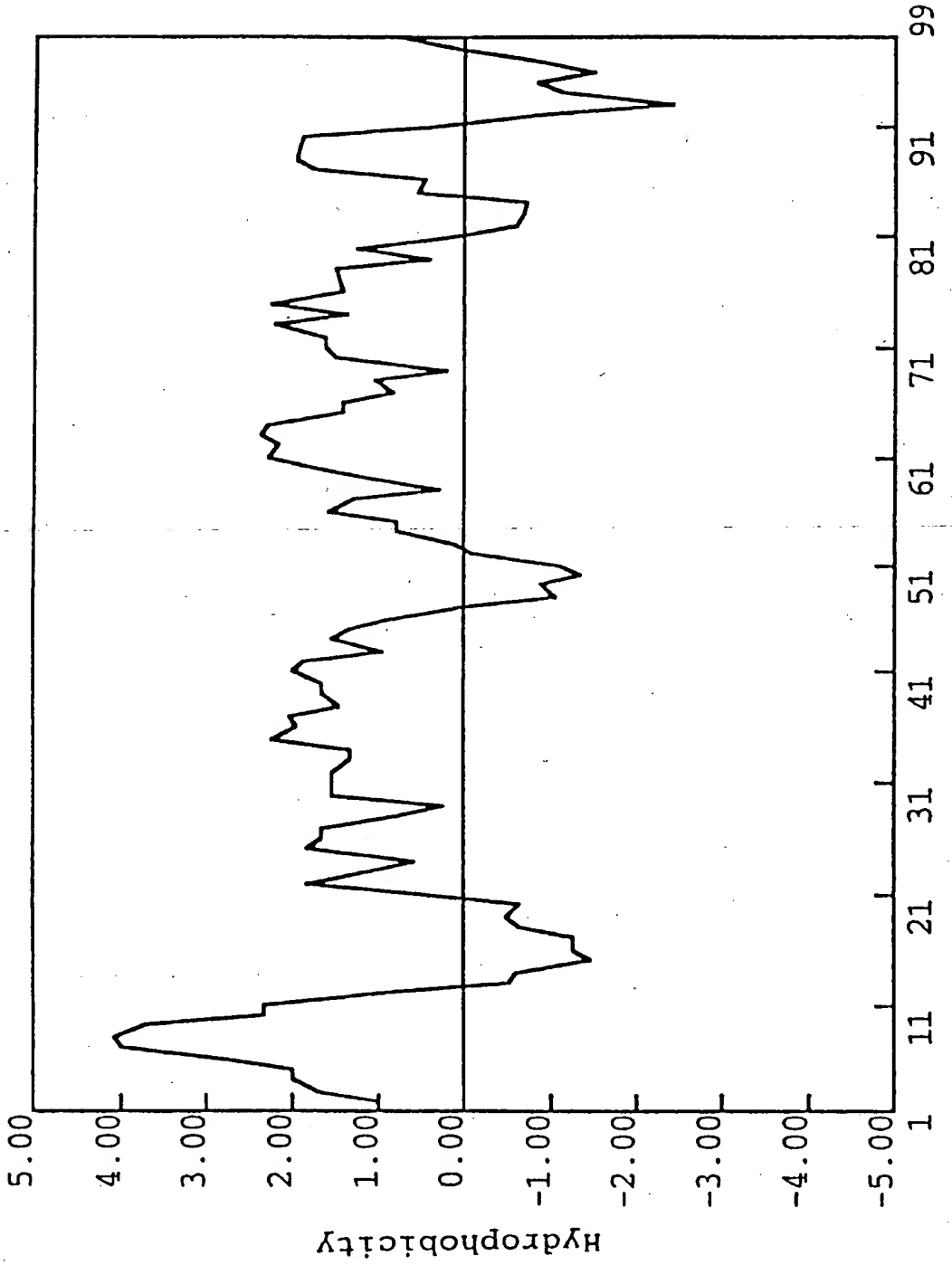

Hydrophobicity
5.00
4.00
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00
-4.00
-5.00
1
11
21
31
41
51
61
71
81
91
99
Position in the amino acid sequence

FIG. 3

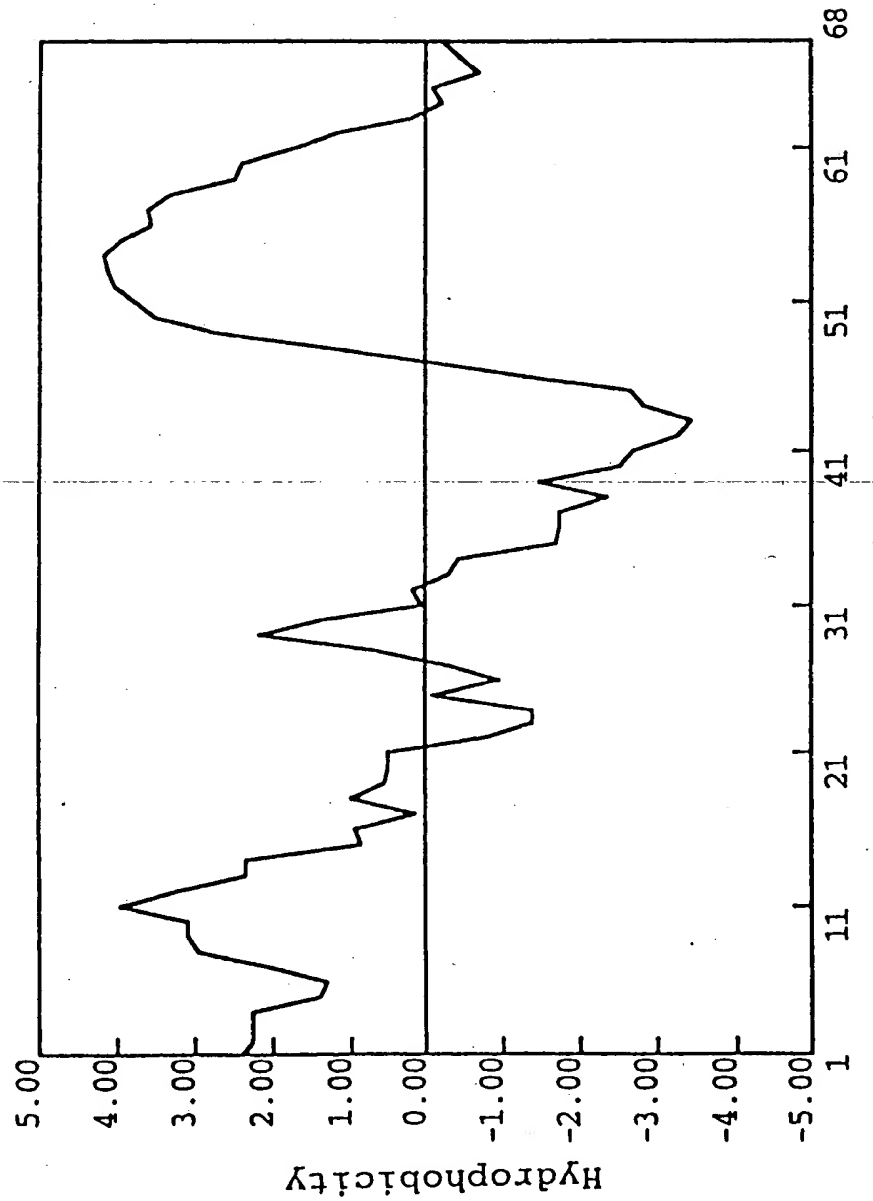

Hydrophobicity
5.00
4.00
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00
-4.00
-5.00
1
11
21
31
41
51
61
68
Position in the amino acid sequence

FIG. 4

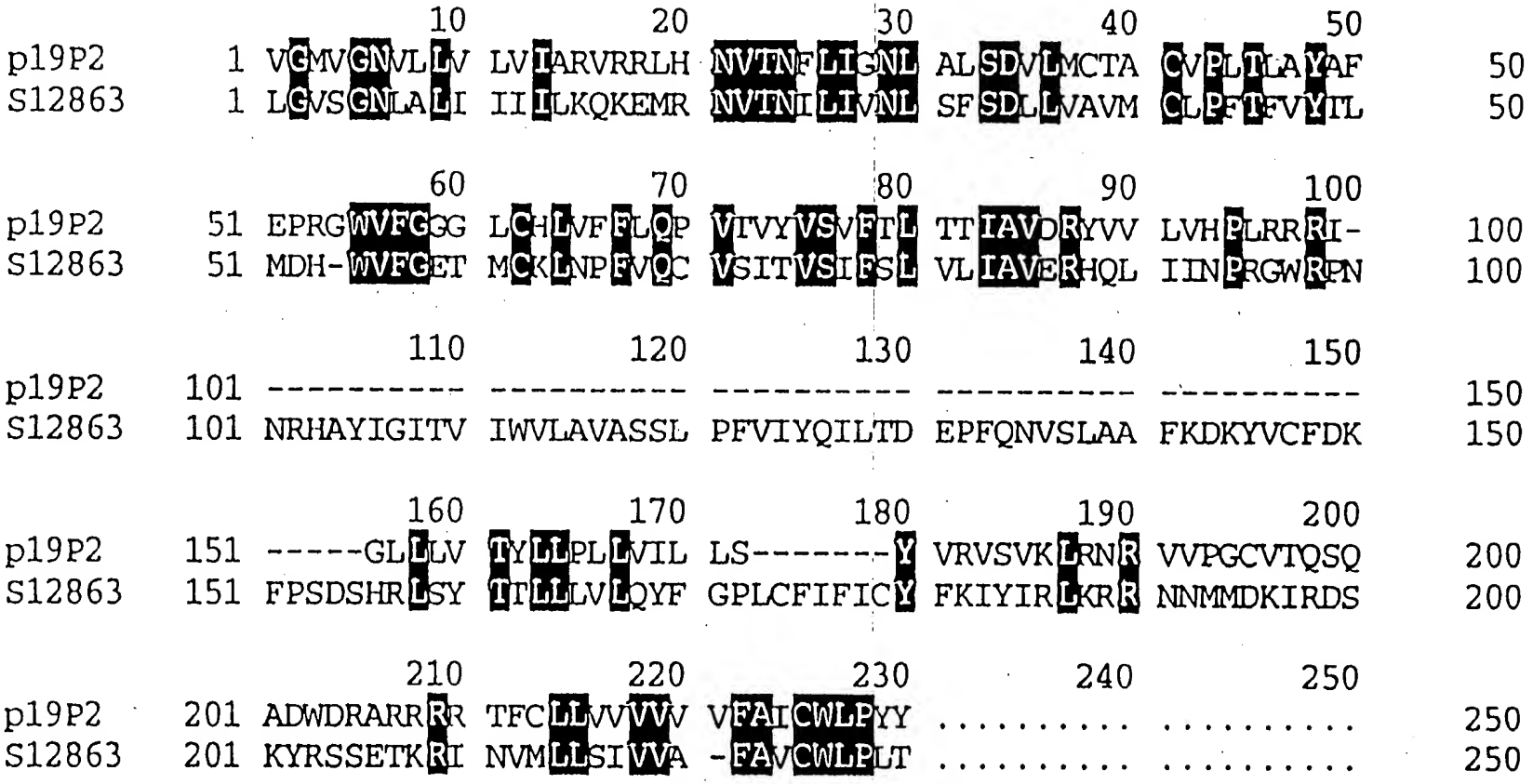

10 20 30 40 50
p19P2 1 VGMVGNVLLV LVIARVRRLH NVTNFLIGNL ALSDVLMCTA CVPLILAYAF 50
S12863 1 LGVSGNLALI IILKQKEMR NVTNILIVNL SFSDLLVAVM CLPFTFVYTL 50
60 70 80 90 100
p19P2 51 EPRGWVFGGG LCHLVFFLQP VIVYVSVFTL TTIAVDRYVV LVHPLRRRI- 100
S12863 51 MDH-WVFGET MCKLNPFVQC VSITVSIFSL VLIAVERHQL IINPRGWRPN 100
110 120 130 140 150
p19P2 101 ---------- ---------- ---------- ---------- ---------- 150
S12863 101 NRHAYIGITV IWVLAVASSL PFVIYQILTD EPFQNVSLAA FKDKYVCFDK 150
160 170 180 190 200
p19P2 151 -----GLLLV TYLLPLLVIL LS-------Y VRVSVKLRNR VVPGCVIQSQ 200
S12863 151 FPSDSHRLSY TILLLVLQYF GPLCFIFICY FKIYIRLKRR NNMMDKIRDS 200
210 220 230 240 250
p19P2 201 ADWDRARRRR TFCLLVVVVV VFAICWLPYY 250
S12863 201 KYRSSETKRI NVMLLSIVVA -FAVCWLPLT 250

FIG. 5

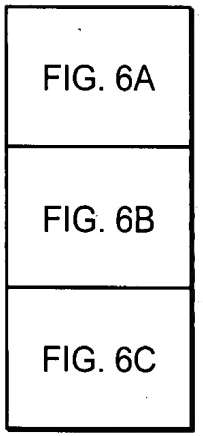


FIG. 6


```
                9          18          27          36          45          54
5'  GTG GGC ATG GTG GGC AAC ATC CTG CTG GTG CTG GTG ATC GCG CGG GTG CGC CGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Gly Met Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg

               63          72          81          90          99          108
    CTG TAC AAC GTG ACG AAT TTC CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu

               117         126         135         144         153         162
    ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT GCC TTC GAG CCA CGC GGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly
```

FIG. 6A

```
        171         180         189         198         207         216
TGG GTG TTC GGC GGC GGC CTG TGC CAC CTG GTC TTC TTC CTG CAG GCG GTC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr

        225         234         243         252         261         270
GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CGC TAC GTC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val

        279         288         297         306         315         324
CTG GTG CAC CCG CTG AGG CGG CGC ATC TCG CTG CGC CTC AGC GCC TAC GCT GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val

        333         342         351         360         369         378
CTG GCC ATC TGG GTG CTG TCC GCG GTG CTG GCG CTG CCC GCC GCC GTG CAC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr

        387         396         405         414         423         432
TAT CAC GTG GAG CTC AAG CCG CAC GAC GTG CGC CTC TGC GAG GAG TTC TGG GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Tyr His Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly
```

FIG. 6B

```
          441           450           459           468           477           486
TCC CAG GAG CGC CAG CGC CAG CTC TAC GCC TGG GGG CTG CTG CTG GTC ACC TAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ser Gln Glu Arg Gln Arg Gln Leu Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr

          495           504           513           522           531           540
CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC GCC CGG GTG TCA GTG AAG CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu

          549           558           567           576           585           594
CGC AAC CGC GTG GTG CCG GGC CGC GTG ACC CAG AGC CAG GCC GAC TGG GAC CGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg

          603           612           621           630           639           648
GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG GTG GTC GTG GTG GTG TTC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Thr

          657           666
CTC TGC TGG CTG CCC TTC TTC 3'
--- --- --- --- --- --- ---
Leu Cys Trp Leu Pro Phe Phe
```

FIG. 6C

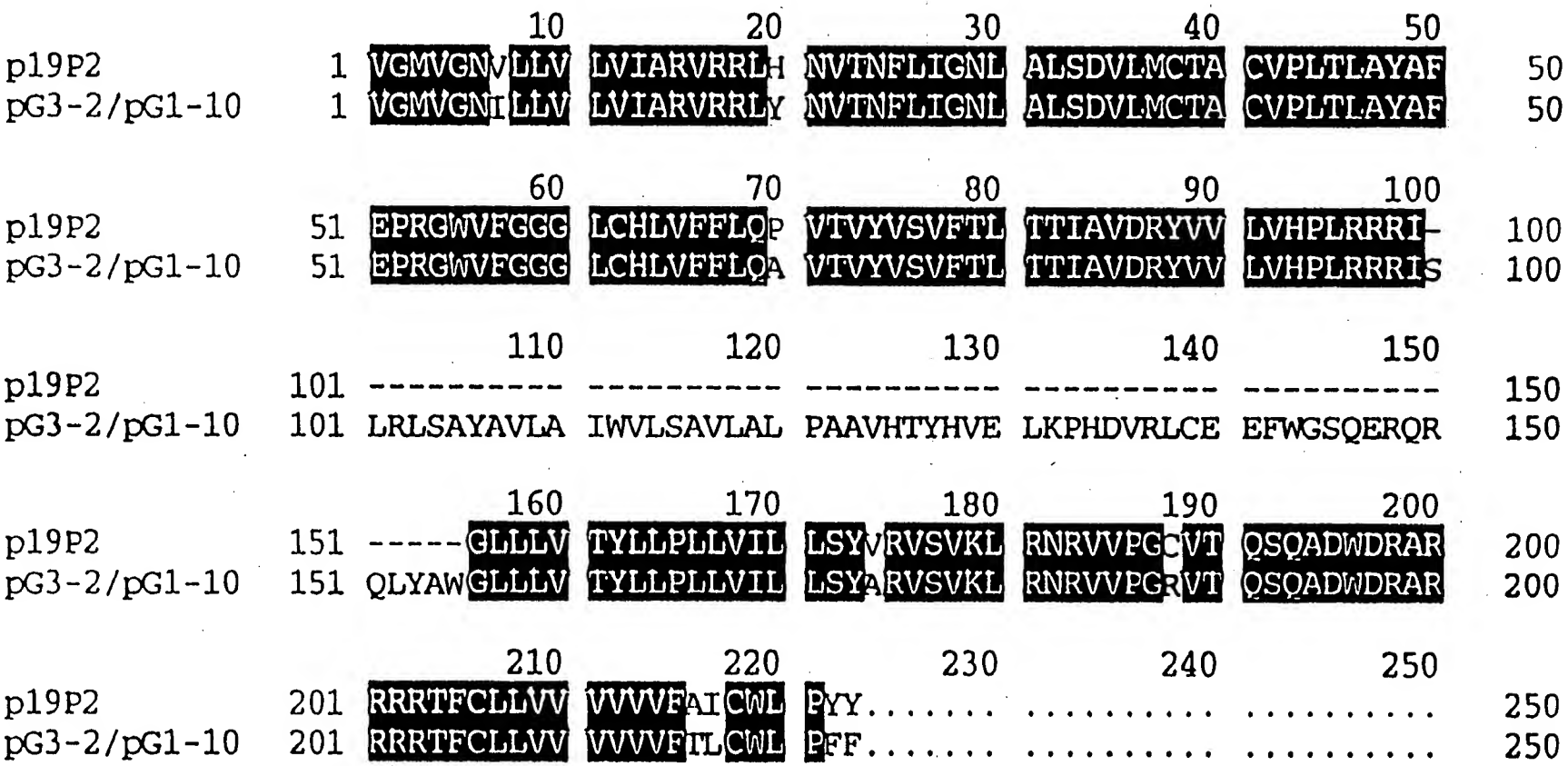

10 20 30 40 50
p19P2 1 VGMVGNVLLV LVIARVRRLH NVTNFLIGNL ALSDVLMCTA CVPLTLAYAF 50
pG3-2/pG1-10 1 VGMVGNILLV LVIARVRRLY NVTNFLIGNL ALSDVLMCTA CVPLTLAYAF 50
60 70 80 90 100
p19P2 51 EPRGWVFGGG LCHLVFFLQP VTVYVSVFTL TTIAVDRYVV LVHPLRRRI- 100
pG3-2/pG1-10 51 EPRGWVFGGG LCHLVFFLQA VTVYVSVFTL TTIAVDRYVV LVHPLRRRIS 100
110 120 130 140 150
p19P2 101 ---------- ---------- ---------- ---------- ---------- 150
pG3-2/pG1-10 101 LRLSAYAVLA IWVLSAVLAL PAAVHTYHVE LKPHDVRLCE EFWGSQERQR 150
160 170 180 190 200
p19P2 151 -----GLLLV TYLLPLLVIL LSYVRVSVKL RNRVVPGCVT QSQADWDRAR 200
pG3-2/pG1-10 151 QLYAWGLLLV TYLLPLLVIL LSYARVSVKL RNRVVPGRVT QSQADWDRAR 200
210 220 230 240 250
p19P2 201 RRRTFCLLVV VVVVFAICWL PYY..... 250
pG3-2/pG1-10 201 RRRTFCLLVV VVVVFTLCWL PFF..... 250

FIG. 7

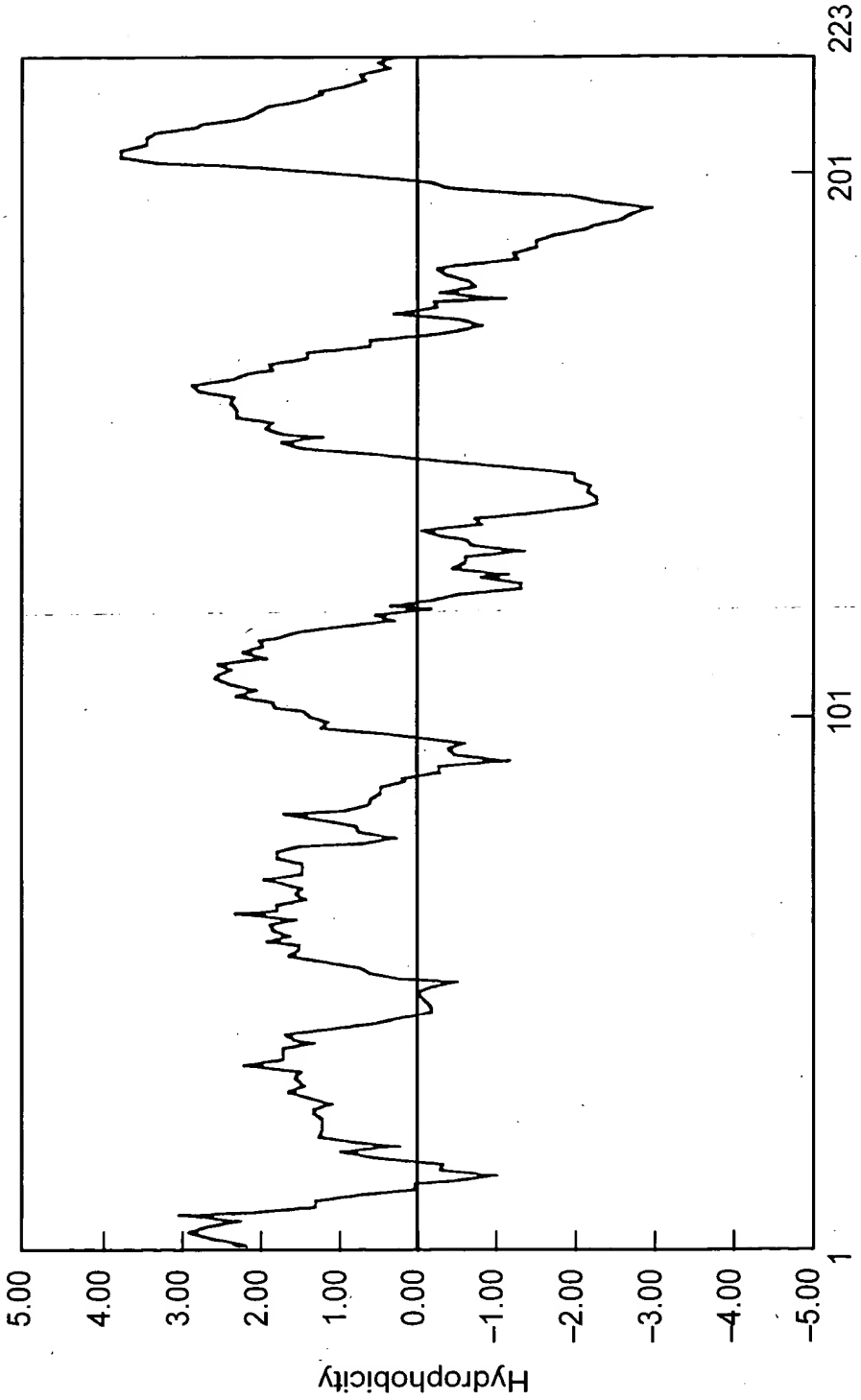

5.00
4.00
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00
-4.00
-5.00
Hydrophobicity
1
101
201
223
Position in the amino acid sequence

FIG. 8

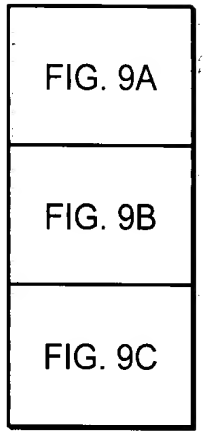


FIG. 9

```
  1 CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGGCCAGCAGAAATT   60
  1                                                                1

 61 CTGCCCCTTCTTCCCGCGAGTGCTTTCCCGCTCTCCAAACCCCACTCCCAGGTGGCCATG  120
  1                                                          Met   1

121 GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTTCTGGGCTGCCGCCGGCG  180
  1 AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla   21

181 GTCACAACTCCCGCCAACCAGAGCGCAGAGGCCTCGGCGGGCAACGGGTCGGTGGCTGGC  240
 21 ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly   41

241 GCGGACGCTCCAGCCGTCACGCCCTTCCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGGG  300
 41 AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly   61
```

FIG. 9A

```
301 CTGATCGTGCTGCTCTACAGCGTCGTGGTGGTCGTGGGGCTGGTGGGCAACTGCCTGCTG 360
 61 LeuIleValLeuLeuTyrSerValValValValValGlyLeuValGlyAsnCysLeuLeu  81

361 GTGCTGGTGATCGCGCGGGTGCGCCGGCTGCACAACGTGACGAACTTCCTCATCGGCAAC 420
 81 ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn 101

421 CTGGCCTTGTCCGACGTGCTCATGTGCACCGCCTGCGTGCCGCTCACGCTGGCCTATGCC 480
101 LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla 121

481 TTCGAGCCACGCGGCTGGGTGTTCGGCGGCGGCCTGTGCCACCTGGTCTTCTTCCTGCAG 540
121 PheGluProArgGlyTrpValPheGlyGlyGlyLeuCysHisLeuValPhePheLeuGln 141

541 CCGGTCACCGTCTATGTGTCGGTGTTCACGCTCACCACCATCGCAGTGGACCGCTACGTC 600
141 ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal 161

601 GTGCTGGTGCACCCGCTGAGGCGGCGCATCTCGCTGCGCCTCAGCGCCTACGCTGTGCTG 660
161 ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu 181

661 GCCATCTGGGCGCTGTCCGCGGTGCTGGCGCTGCCCGCCGCCGTGCACACCTATCACGTG 720
181 AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal 201

721 GAGCTCAAGCCGCACGACGTGCGCCTCTGCGAGGAGTTCTGGGGCTCCCAGGAGCGCCAG 780
201 GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln 221

781 CGCCAGCTCTACGCCTGGGGGCTGCTGCTGGTCACCTACCTGCTCCCTCTGCTGGTCATC 840
221 ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle 241
```

FIG. 9B

```
 841 CTCCTGTCTTACGTCCGGGTGTCAGTGAAGCTCCGCAACCGCGTGGTGCCGGGCTGCGTG   900
 241 LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal   261

 901 ACCCAGAGCCAGGCCGACTGGGACCGCGCTCGGCGCCGGCGCACCTTCTGCTTGCTGGTG   960
 261 ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgArgThrPheCysLeuLeuVal   281

 961 GTGGTCGTGGTGGTGTTCGCCGTCTGCTGGCTGCCGCTGCACGTCTTCAACCTGCTGCGG  1020
 281 ValValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg   301

1021 GACCTCGACCCCCACGCCATCGACCCTTACGCCTTTGGGCTGGTGCAGCTGCTCTGCCAC  1080
 301 AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis   321

1081 TGGCTCGCCATGAGTTCGGCCTGCTACAACCCCTTCATCTACGCCTGGCTGCACGACAGC  1140
 321 TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer   341

1141 TTCCGCGAGGAGCTGCGCAAACTGTTGGTCGCTTGGCCCCGCAAGATAGCCCCCCATGGC  1200
 341 PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly   361

1201 CAGAATATGACCGTCAGCGTGGTCATCTGATGCCACTTAGCCAGGCCTTGGTCAAGGAGC  1260
 361 GlnAsnMetThrValSerValValIle***                                  371

1261 TCCACTTCAACTGGCCTCCTAGGGCACCACTCGAGGTCAATCTGGTGCTTATTCTCAGCA  1320
 371                                                                371

1321 CCAGAGCTAGC                                                    1331
 371                                                                371
```

FIG. 9C

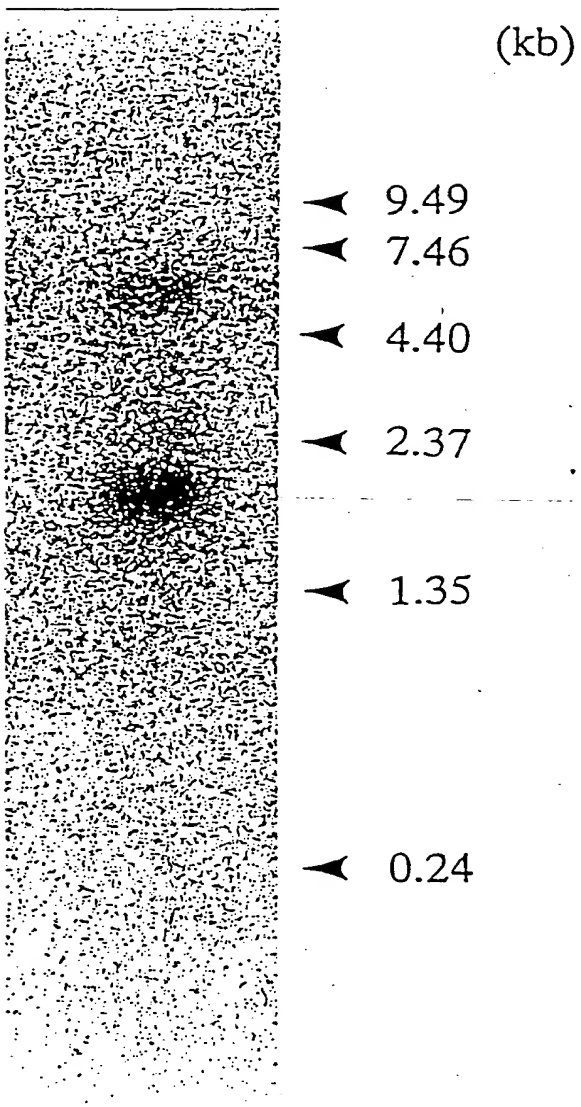
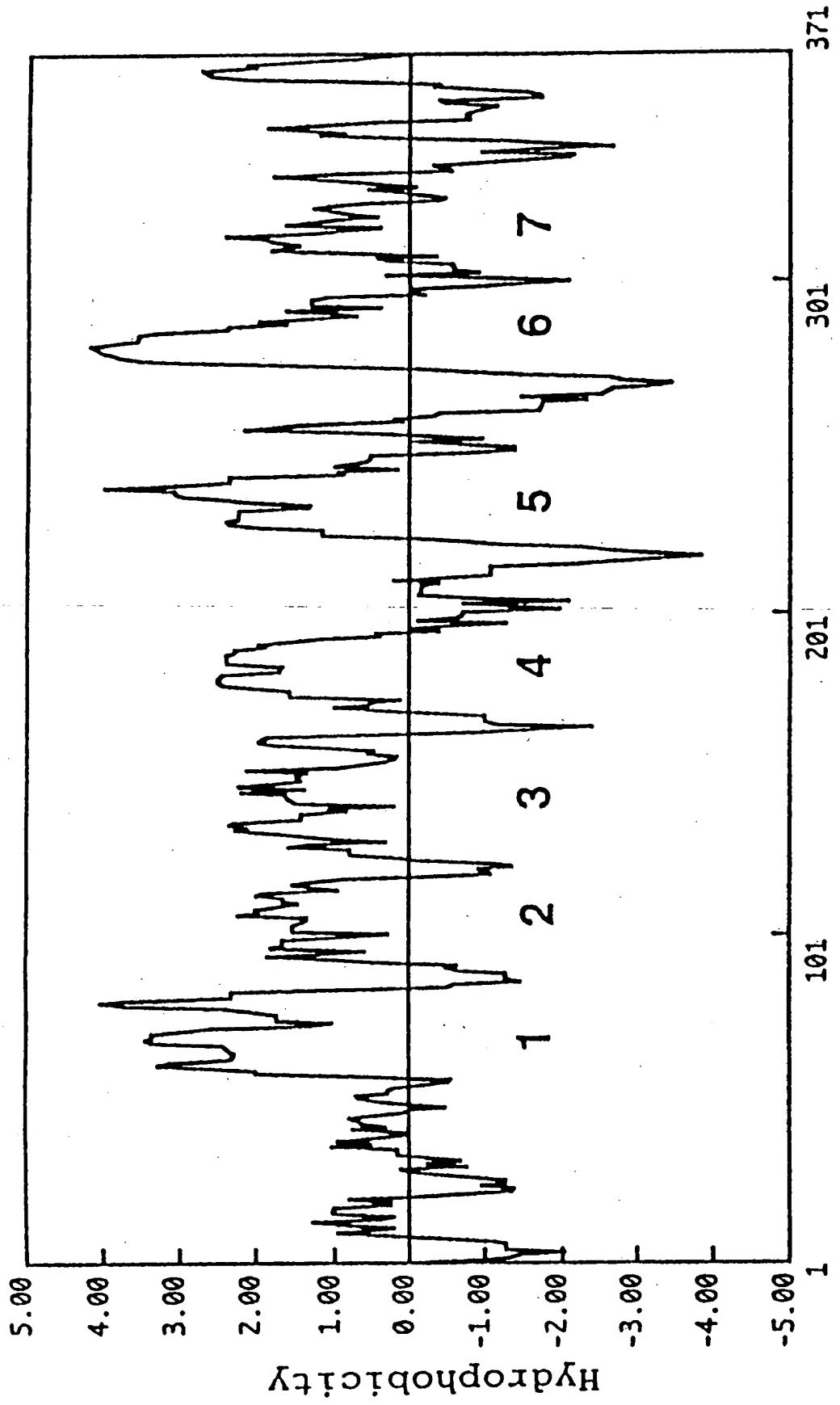


FIG. 10


Hydrophobicity
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4.00
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00
-4.00
-5.00
1
101
201
301
371
Position in the amino acid sequence
1
2
3
4
5
6
7

FIG. 11

```
                9          18          27          36          45          54
5'  CTG TGT GTC ATC GCG GTG GAT AGG TAC GTG GTT CTG GTG CAC CCG CTA CGT CGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Cys Val Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg Arg

               63          72          81          90          99         108
    CGC ATT TCA CTG AGG CTC AGC GCC TAC GCG GTG CTG GGC ATC TGG GCT CTA TCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser

              117         126         135         144         153         162
    GCA GTG CTG GCG CTG CCG GCC GCG GTG CAC ACC TAC CAT GTG GAG CTC AAG CCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro

              171         180         189         198         207         216
    CAC GAC GTG AGC CTC TGC GAG GAG TTC TGG GGC TCG CAG GAG CGC CAA CGC CAG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    His Asp Val Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln

              225         234         243         252         261         270
    ATC TAC GCC TGG GGG CTG CTT CTG GGC ACC TAT TTG CTC CCC CTG CTG GCC ATC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala Ile

              279         288         297         306         315         324
    CTC CTG TCT TAC GTA CGG GTG TCA GTG AAG CTG AGG AAC CGC GTG GTG CCT GGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly

              333         342         351         360         369         378
    AGC GTG ACC CAG AGT CAA GCT GAC TGG GAC CGA GCG CGT CGC CGC CGC ACT TTC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe

              387         396         405         414         423         432
    TGT CTG CTG GTG GTG GTG GTG GTA GTG TTC ACG CTC TGC TGG CTG CCC TTC TAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Cys Leu Leu Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Tyr

    CT 3'
    --
    —
```

FIG. 12

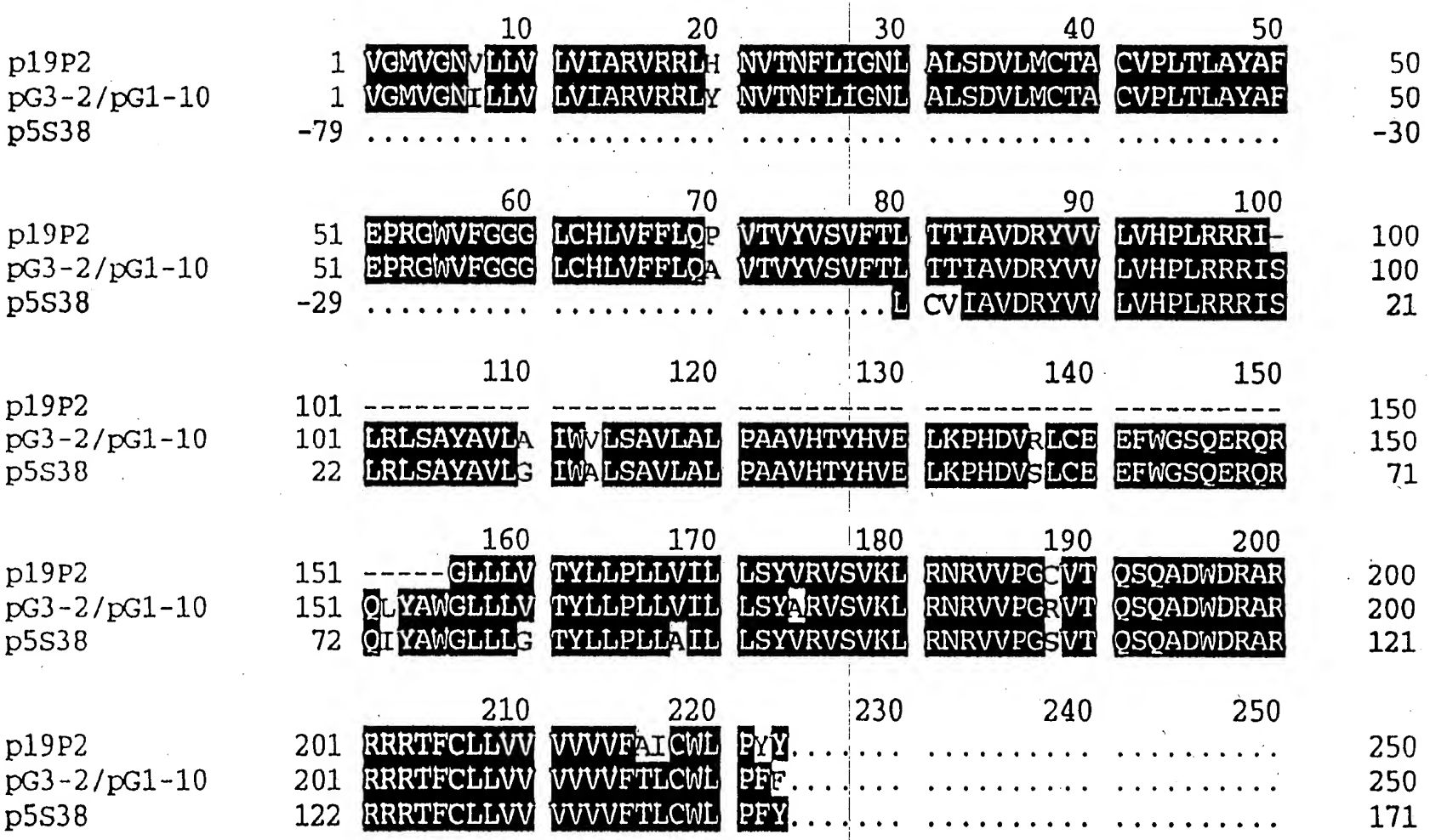

10 20 30 40 50
p19P2 1 VGMVGNVLLV LVIARVRRLH NVTNFLIGNL ALSDVLMCTA CVPLTLAYAF 50
pG3-2/pG1-10 1 VGMVGNILLV LVIARVRRLY NVTNFLIGNL ALSDVLMCTA CVPLTLAYAF 50
p5S38 -79 .... -30
60 70 80 90 100
p19P2 51 EPRGWVFGGG LCHLVFFLQP VTVYVSVFTL TTIAVDRYVV LVHPLRRRI- 100
pG3-2/pG1-10 51 EPRGWVFGGG LCHLVFFLQA VTVYVSVFTL TTIAVDRYVV LVHPLRRRIS 100
p5S38 -29 ....L CVIAVDRYVV LVHPLRRRIS 21
110 120 130 140 150
p19P2 101 ---------- ---------- ---------- ---------- ---------- 150
pG3-2/pG1-10 101 LRLSAYAVLA IWVLSAVLAL PAAVHTYHVE LKPHDVRLCE EFWGSQERQR 150
p5S38 22 LRLSAYAVLG IWALSAVLAL PAAVHTYHVE LKPHDVSLCE EFWGSQERQR 71
160 170 180 190 200
p19P2 151 -----GLLLV TYLLPLLVIL LSYVRVSVKL RNRVVPGCVT QSQADWDRAR 200
pG3-2/pG1-10 151 QLYAWGLLLV TYLLPLLVIL LSYARVSVKL RNRVVPGRVT QSQADWDRAR 200
p5S38 72 QIYAWGLLLG TYLLPLLAIL LSYVRVSVKL RNRVVPGSVT QSQADWDRAR 121
210 220 230 240 250
p19P2 201 RRRTFCLLVV VVVVFAICWL PYY..... 250
pG3-2/pG1-10 201 RRRTFCLLVV VVVVFTLCWL PFF..... 250
p5S38 122 RRRTFCLLVV VVVVFTLCWL PFY..... 171

FIG. 13

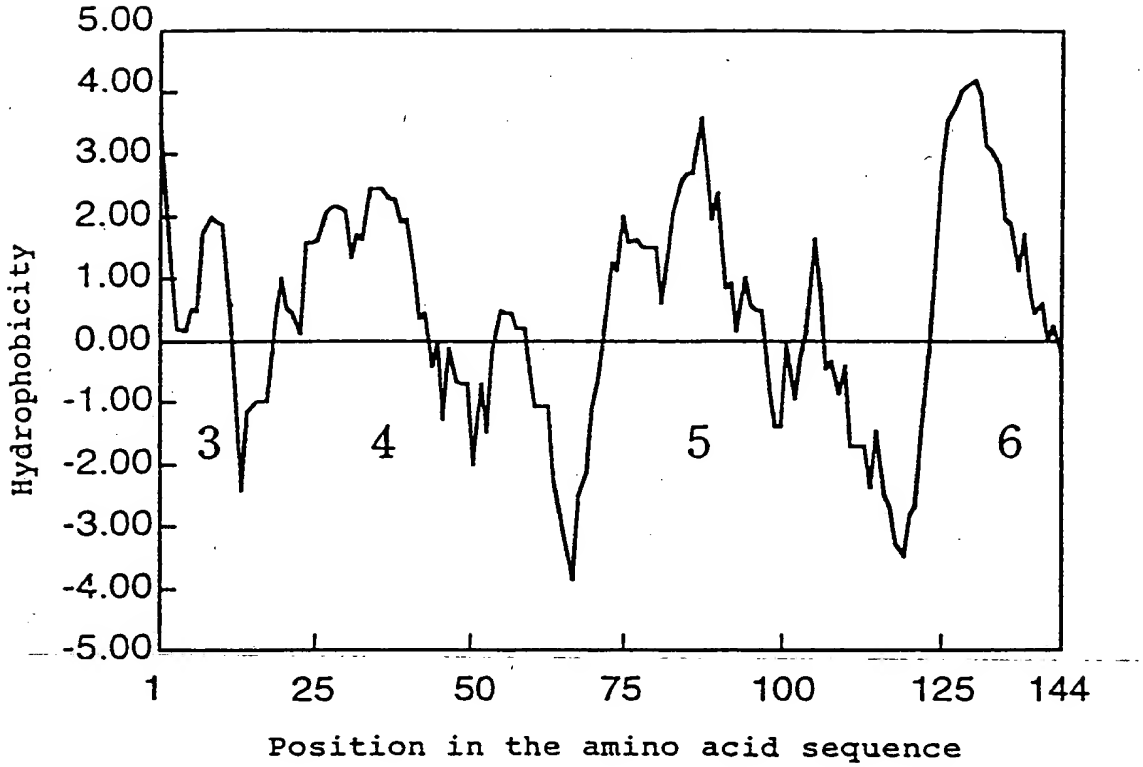

5.00
4.00
3.00
2.00
1.00
0.00
-1.00
-2.00
-3.00
-4.00
-5.00
Hydrophobicity
3
4
5
6
1
25
50
75
100
125
144
Position in the amino acid sequence

FIG. 14

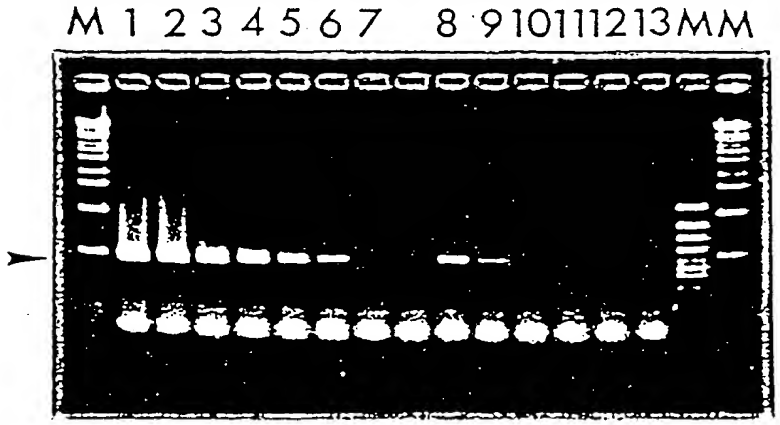
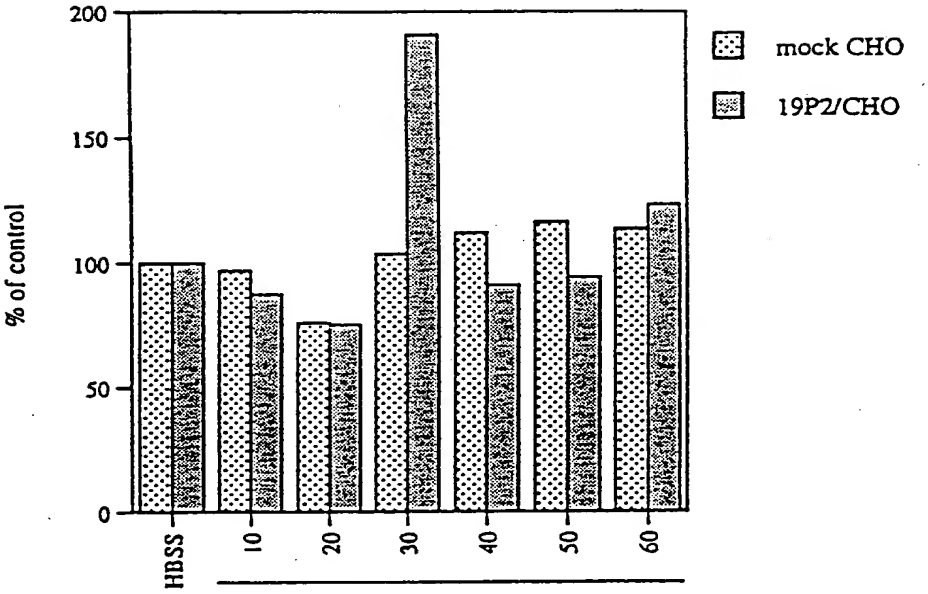
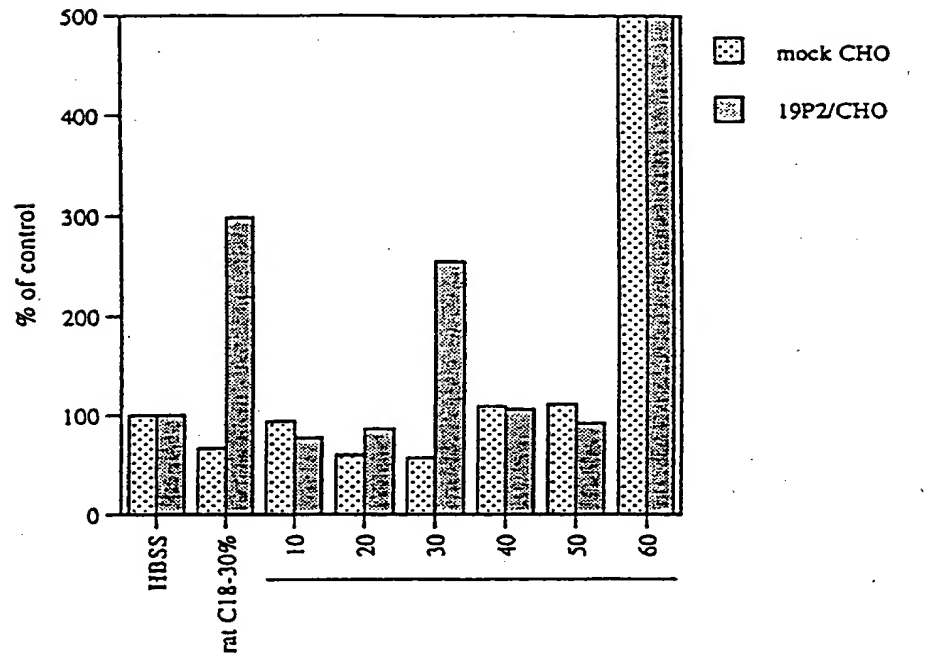

M 1 2 3 4 5 6 7 8 9 10 11 12 13 M M

FIG. 15



rat whole brain extract
C_{18}-column CH_3CN elution (%)

FIG. 16



bovine hypothalamus extract
C_{18}-column CH_3CN elution (%)

FIG. 17

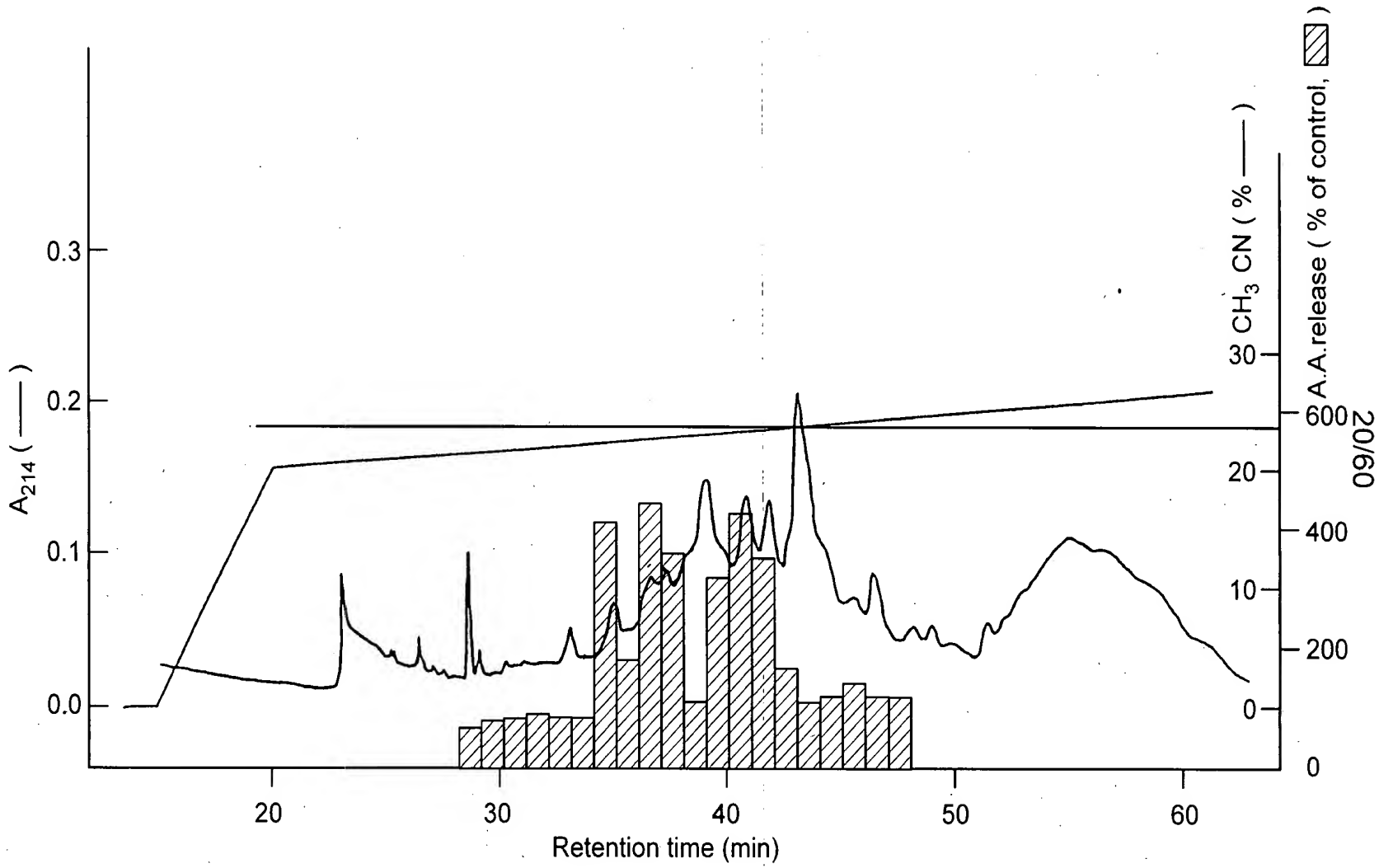

0.3
0.2
0.1
0.0
A_{214} (——)
20
30
40
50
60
Retention time (min)
30
20
10
0
CH_3 CN (% ——)
600
400
200
0
A.A.release (% of control, ▨)
20/60

FIG. 18

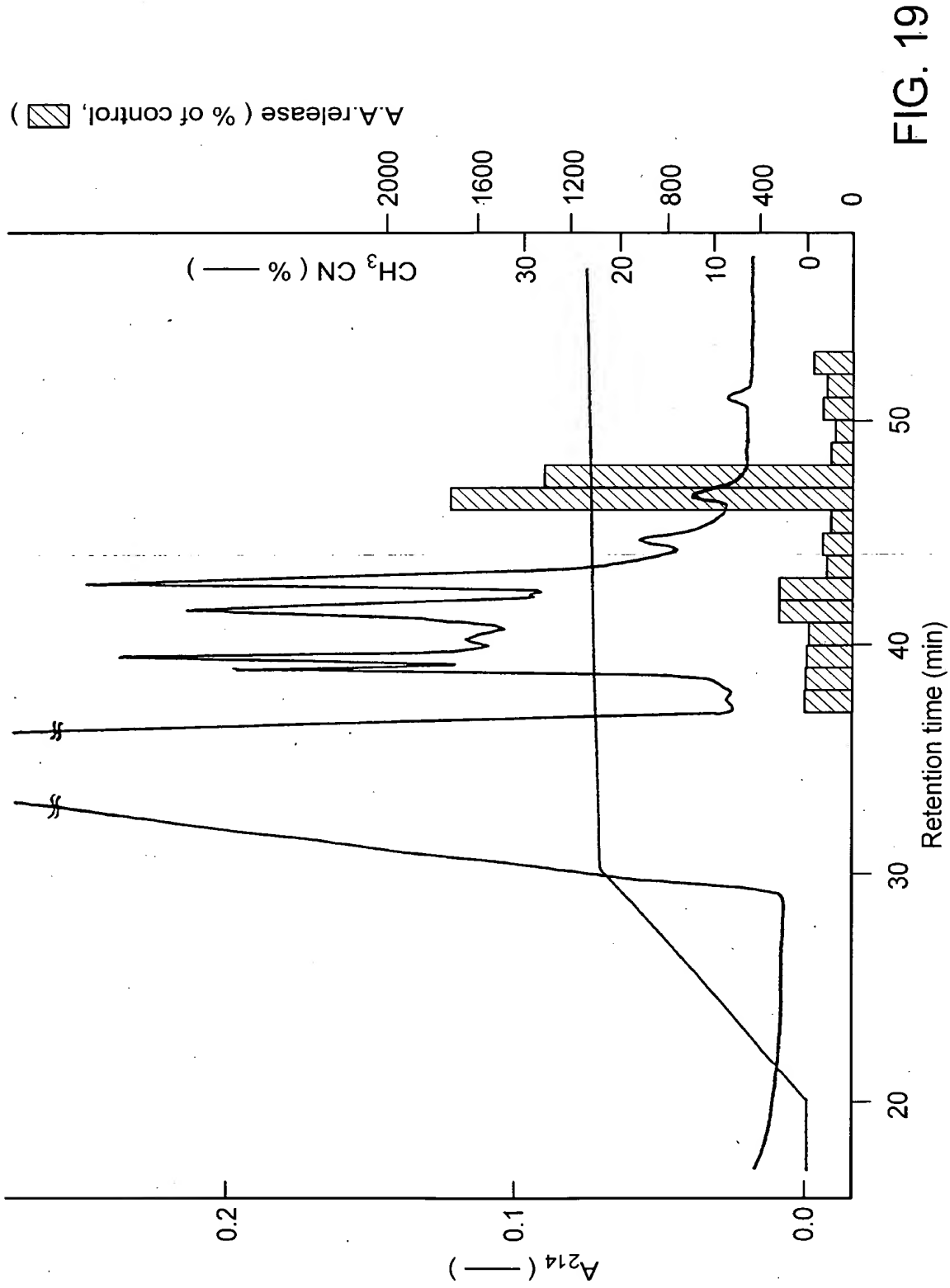

A214 (——)
0.0
0.1
0.2
20
30
40
50
Retention time (min)
CH3 CN (% ——)
0
10
20
30
0
400
800
1200
1600
2000
A.A.release (% of control, ▨)

FIG. 19

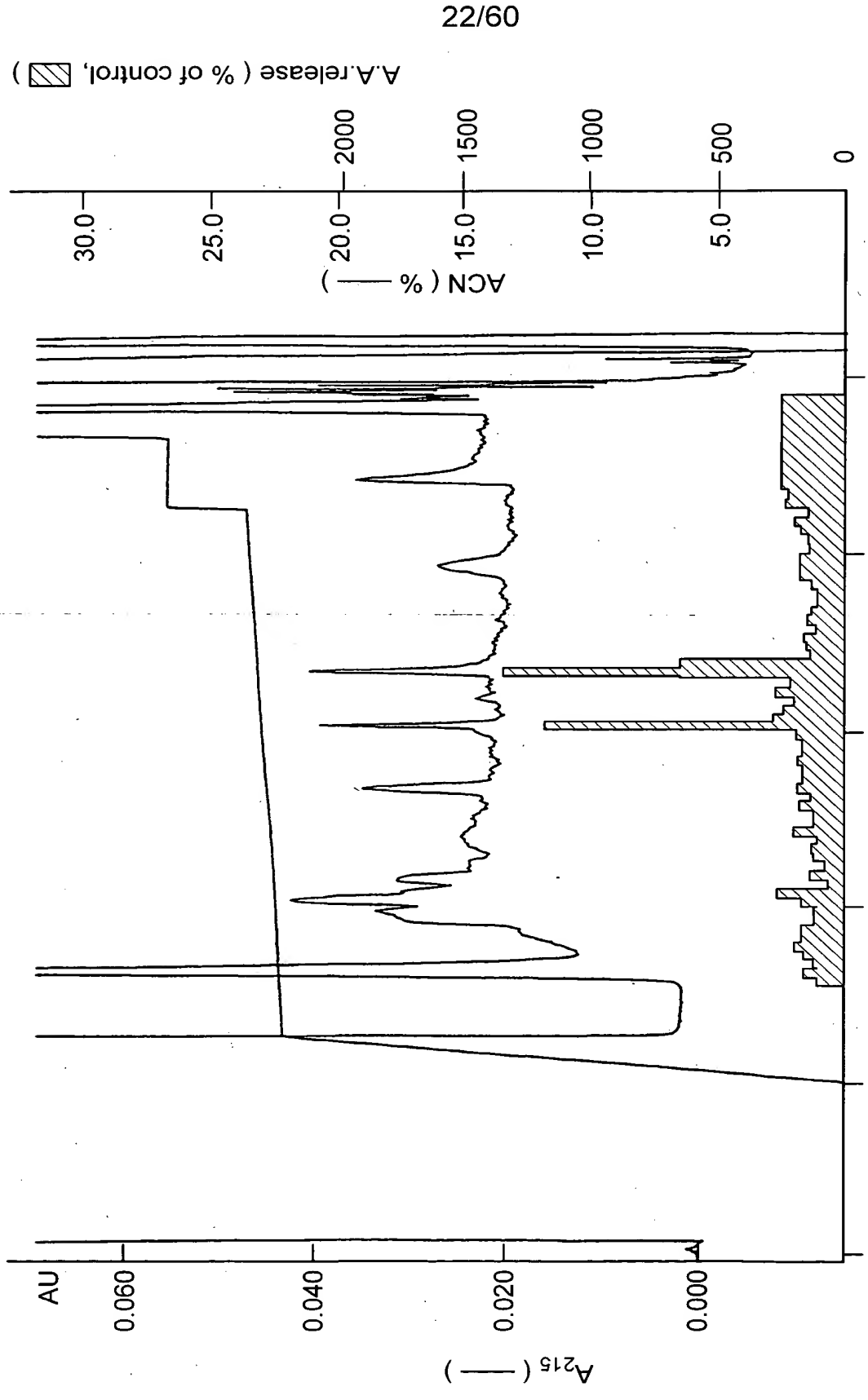

A.A.release (% of control, ▨)
ACN (% ——)
30.0
25.0
20.0
15.0
10.0
5.0
2000
1500
1000
500
0
A215 (——)
AU
0.060
0.040
0.020
0.000
0
20
40
60
80
100 min
Retention time (min)

FIG. 20

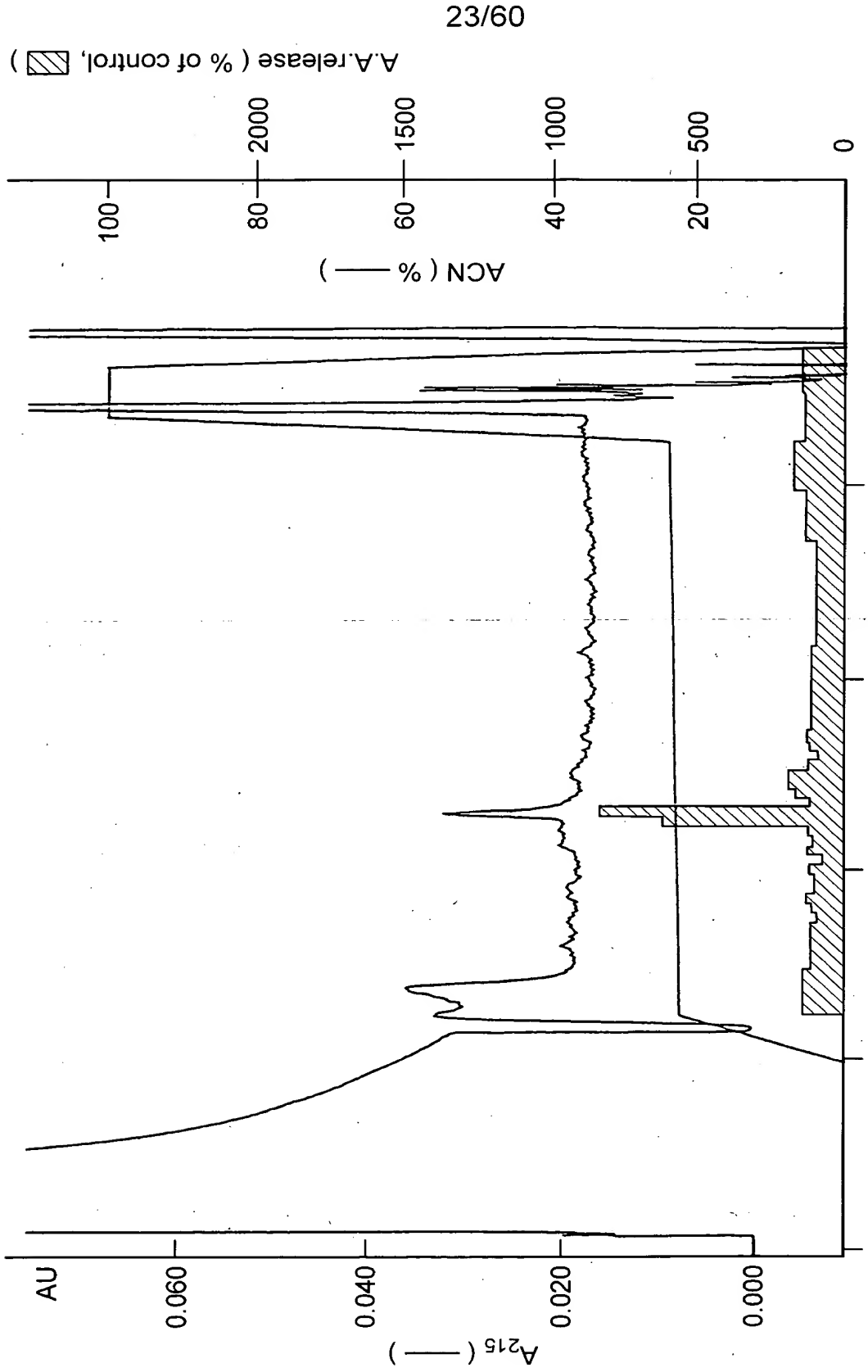

A215 (——)
AU
0.060
0.040
0.020
0.000
0
20
40
60
80
Retention time (min)
ACN (% ——)
100
80
60
40
20
2000
1500
1000
500
0
A.A.release (% of control, ▨)

FIG. 21

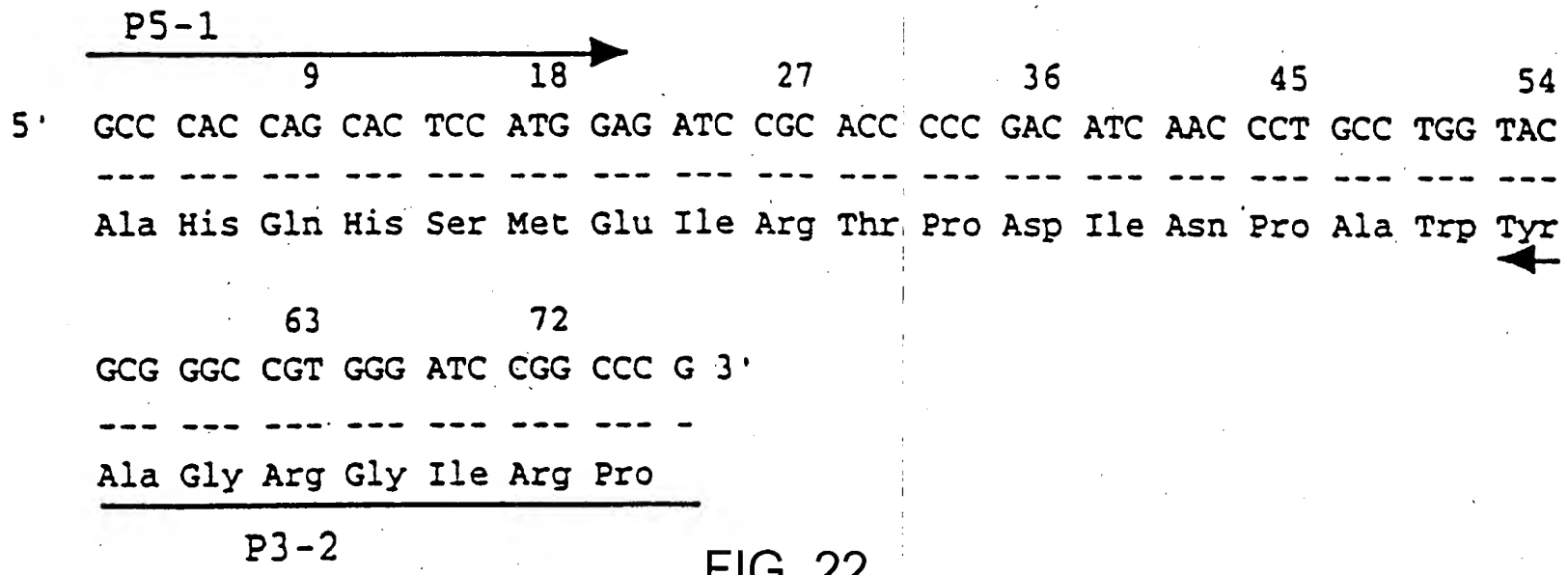

P5-1
9
18
27
36
45
54
5' GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC
Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr
63
72
GCG GGC CGT GGG ATC CGG CCC G 3'
Ala Gly Arg Gly Ile Arg Pro
P3-2

FIG. 22

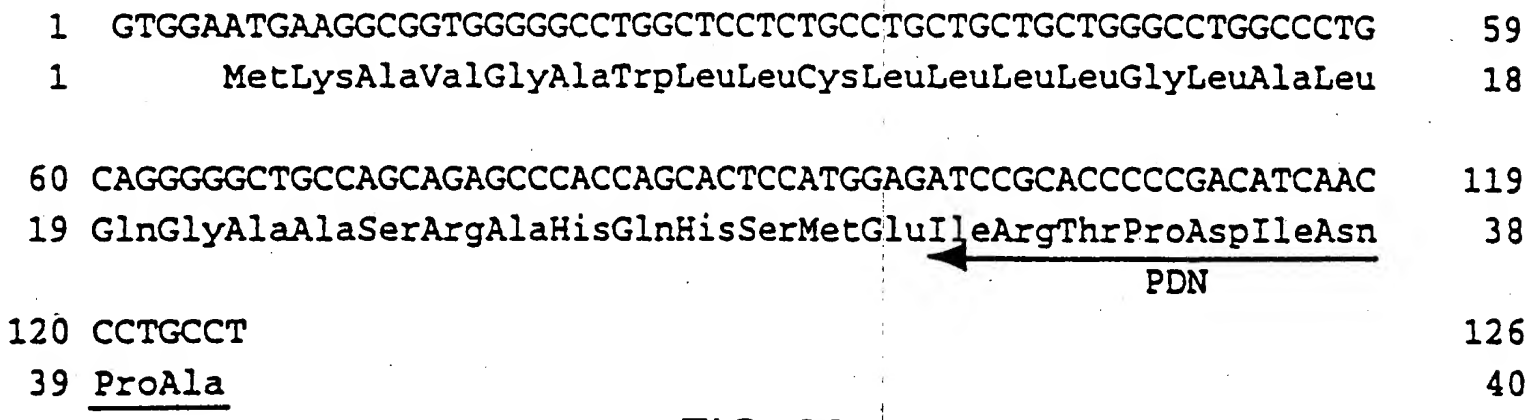

1 GTGGAATGAAGGCGGTGGGGGCCTGGCTCCTCTGCCTGCTGCTGCTGGGCCTGGCCCTG 59
1 MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu 18
60 CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC 119
19 GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn 38
PDN
120 CCTGCCT 126
39 ProAla 40

FIG. 23

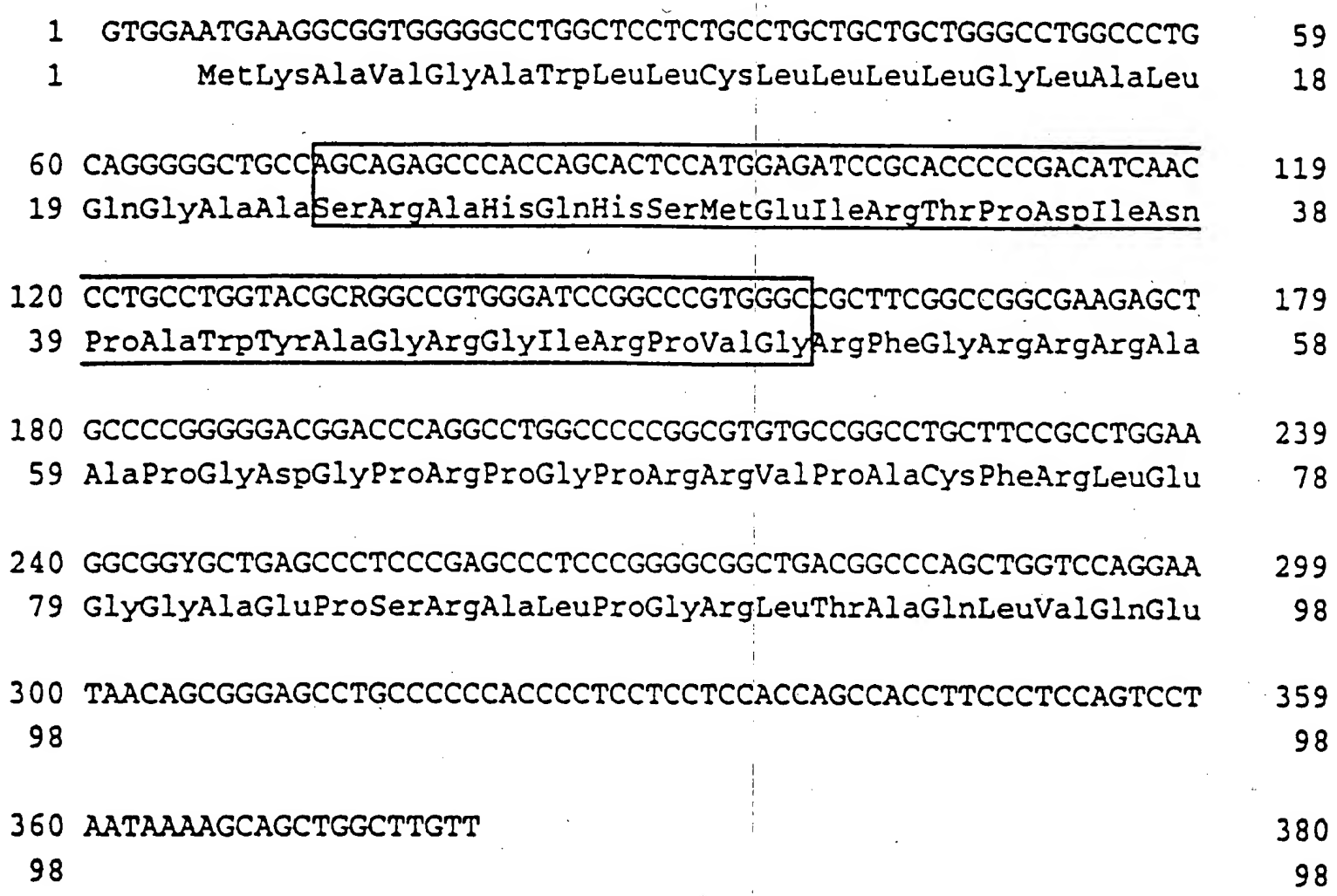

1 GTGGAATGAAGGCGGTGGGGGCCTGGCTCCTCTGCCTGCTGCTGCTGGGCCTGGCCCTG 59
1 MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu 18
60 CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC 119
19 GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn 38
120 CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCGTGGGCCGCTTCGGCCGGCGAAGAGCT 179
39 ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgArgAla 58
180 GCCCCGGGGGACGGACCCAGGCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCTGGAA 239
59 AlaProGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu 78
240 GGCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGCGGCTGACGGCCCAGCTGGTCCAGGAA 299
79 GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu 98
300 TAACAGCGGGAGCCTGCCCCCCACCCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT 359
98 98
360 AATAAAAGCAGCTGGCTTGTT 380
98 98

FIG. 24A

```
  1  GTGGAATGAAGGCGGTGGGGGCCTGGCTCCTCTGCCTGCTGCTGCTGGGCCTGGCCCTG     59
  1       MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu     18

 60 CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC    119
 19 GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn     38

120 CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCGTGGGCCGCTTCGGCCGGCGAAGAGCT    179
 39 ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgArgAla     58

180 GCCCTGGGGGACGGACCCAGGCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCTGGAA    239
 59 AlaLeuGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu     78

240 GGCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGCGGCTGACGGCCCAGCTGGTCCAGGAA    299
 79 GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu     98

300 TAACAGCGGGAGCCTGCCCCCCACCCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT    359
 98                                                                 98

360 AATAAAAGCAGCTGGCTTGTT                                         380
 98                                                                 98
```

FIG. 24B

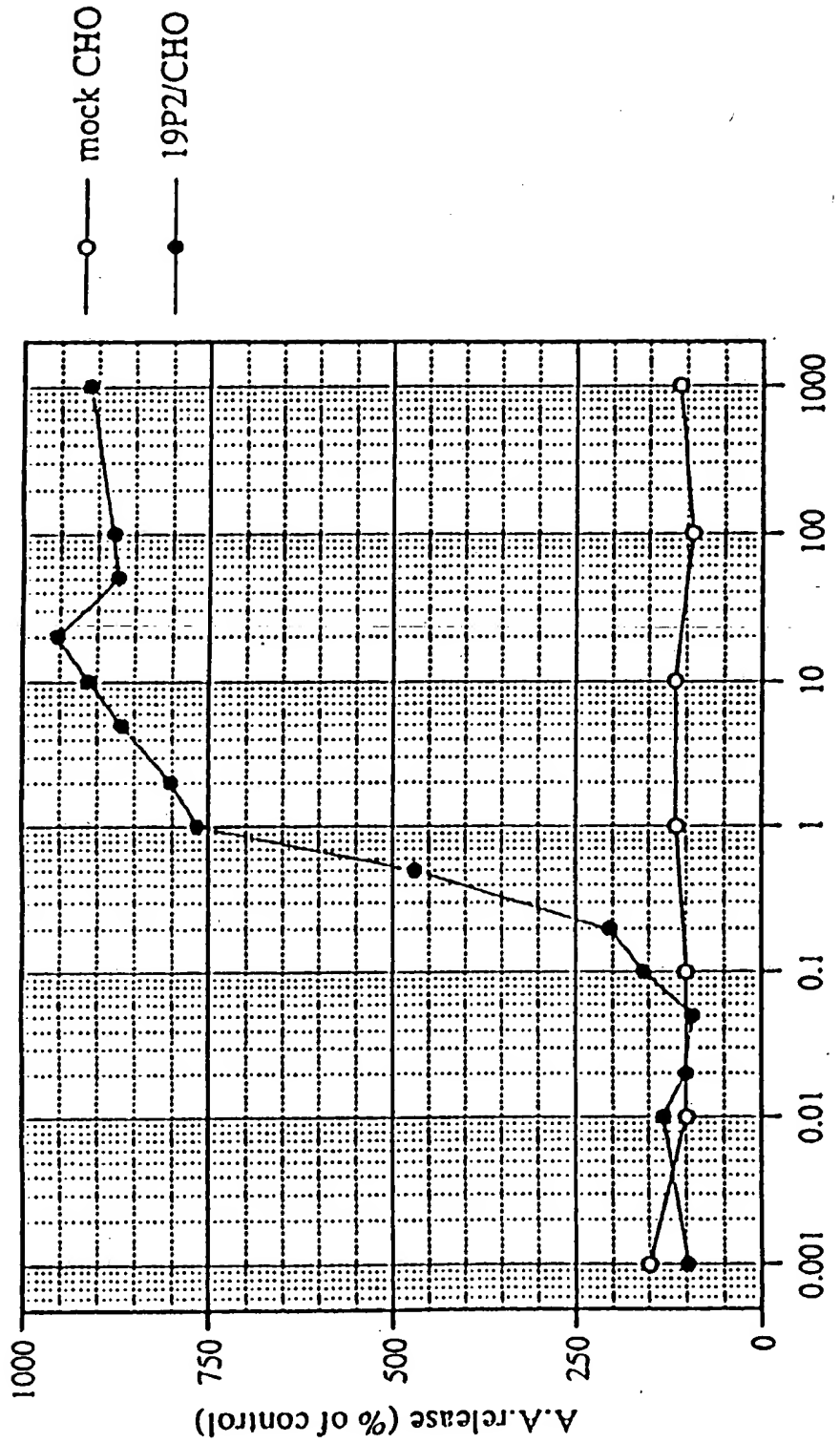

mock CHO
19P2/CHO
A.A.release (% of control)
1000
750
500
250
0
0.001
0.01
0.1
1
10
100
1000
Peptide conc. (x10⁻⁹M)

FIG. 25

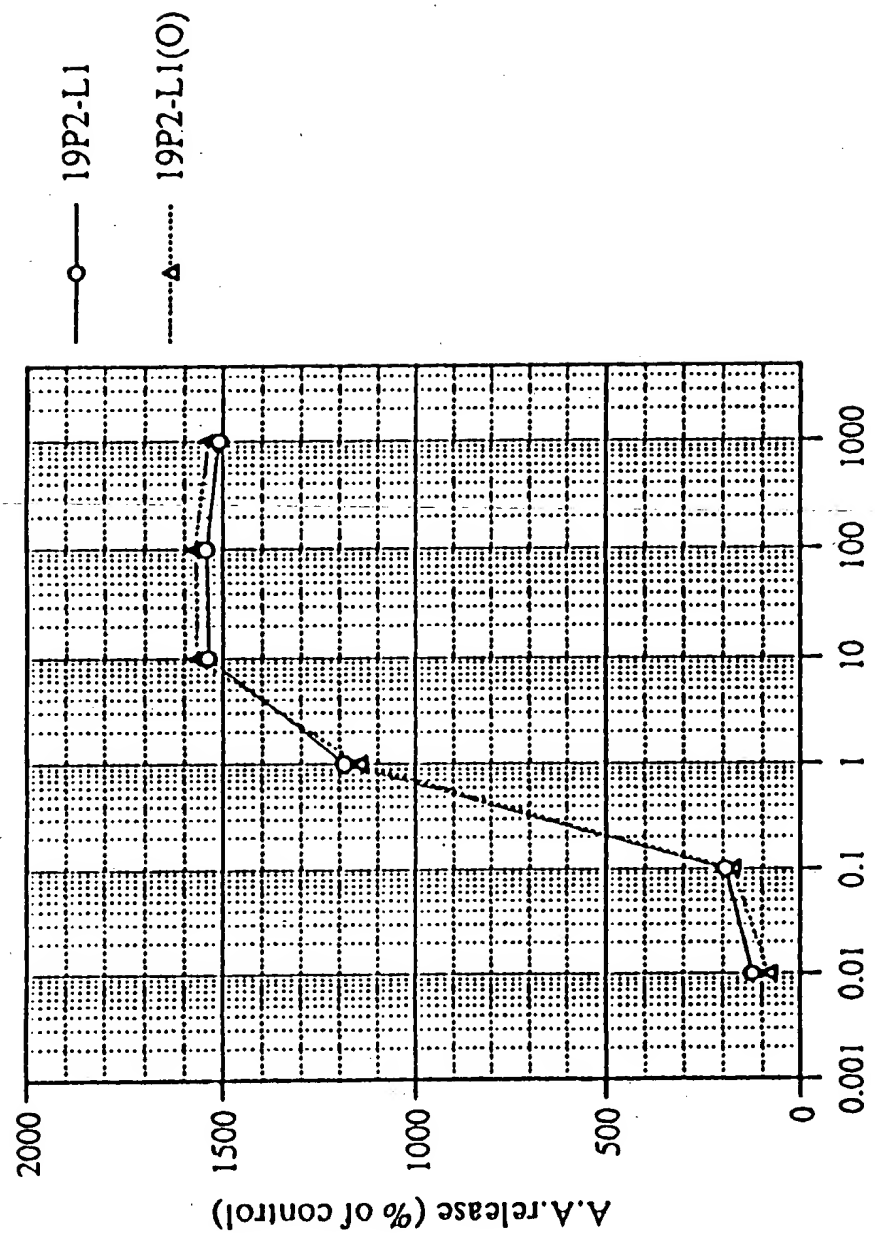

19P2-L1
19P2-L1(O)
A.A.release (% of control)
2000
1500
1000
500
0
0.001
0.01
0.1
1
10
100
1000
Peptide conc. (x 10^{-9}M)

FIG. 26

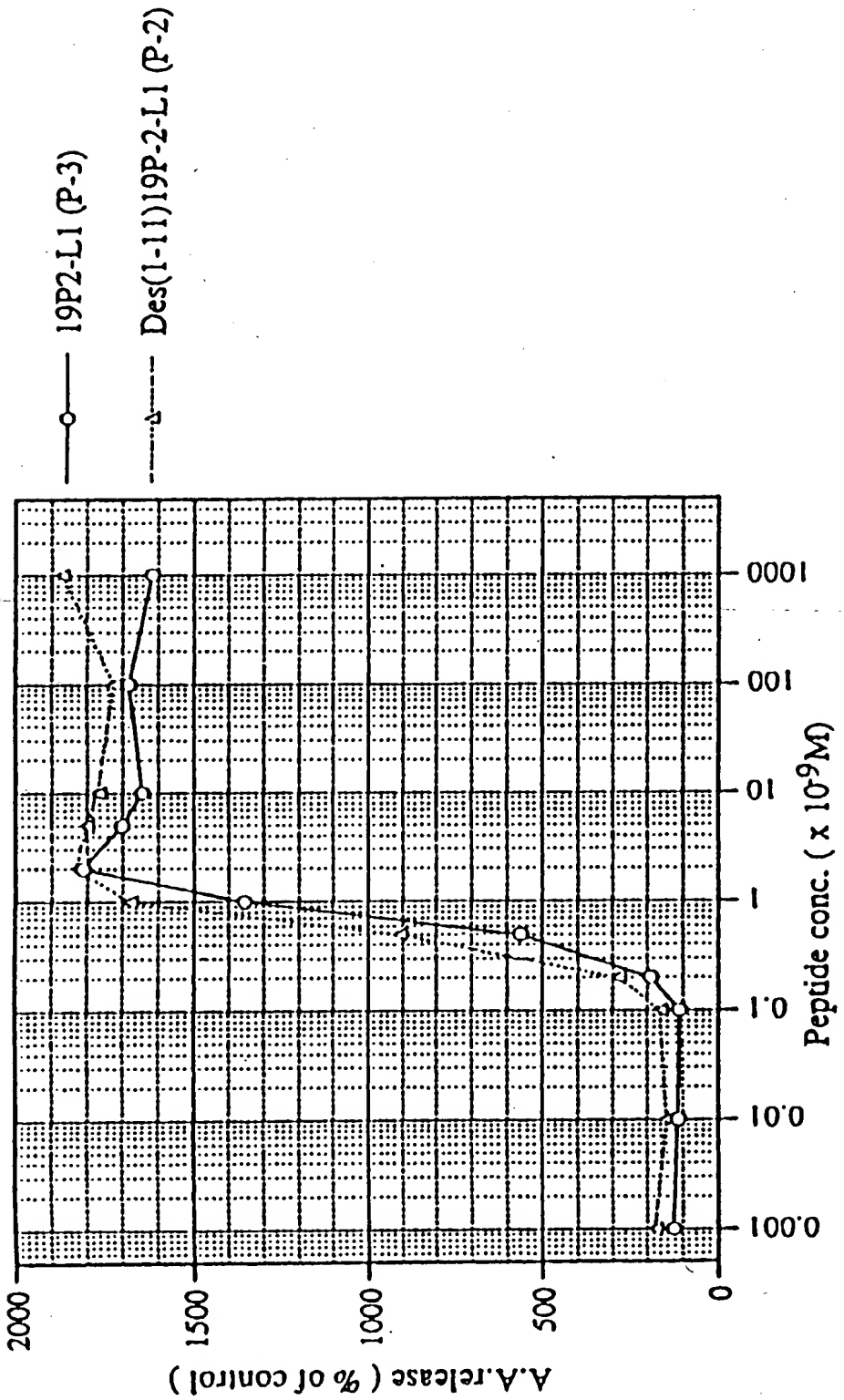

19P2-L1 (P-3)
Des(1-11)19P-2-L1 (P-2)
A.A.release (% of control)
2000
1500
1000
500
0
Peptide conc. (x 10^{-9}M)
1000
100
10
1
0.1
0.01
0.001

FIG. 27

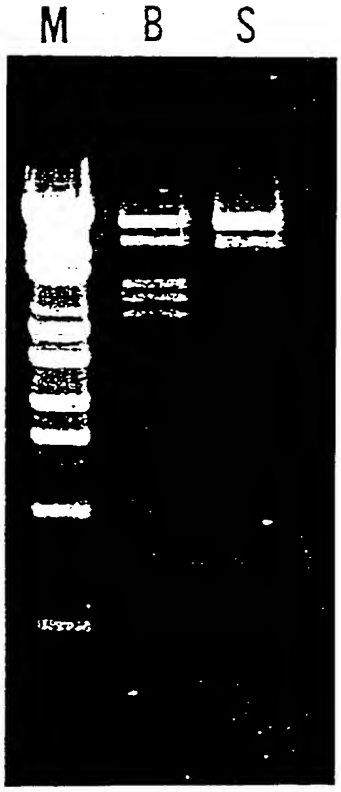


FIG. 28

```
        10         20         30         40         50         60
ATGAAGGCGG TGGGGGCCTG GCTCCTCTGC CTGCTGCTGC TGGGCCTGGC CCTGCAGGGG

        70         80         90        100        110        120
GCTGCCAGCA GAGCCCACCA GCACTCCATG GAGATCCGCA GTGAGTGTCT AGCCCCGCCC

       130        140        150        160        170        180
CTGCCCCCAG GGGTCACAGG GGGGGCCTGG CCACTTCCTG GGCTGGGACA TCCTTGCTAA

       190        200        210        220        230        240
GCATCCTGGG GTTGGGGTTT GGCCTCCTGT TCCCCAGACC CTTCCCCCAG GTGGCCCGGA

       250        260        270        280        290        300
CAGGTGCTCC CAAGGGTCCC GGCCCAGCAC ACGGGGGAGG GTCACTCCTC ACCACACGGG

       310        320        330        340        350        360
TGGCGTGGGG CTGAGTGCAC GTCACCCATG AGAACGGGGC TGTGAGGACA GGAAAGGAAG

       370        380        390        400        410        420
GGGAGTGTGT CCTGGTGTGA GTCTGAAATC CTACTTCCCA AAGCCACCCC AGCACCAGAA

       430        440        450        460        470        480
ATGGGCGCTC CGGGTGAACC TCCTGTGCGG GTGGGTGGTC CTGGCATGGC CTGGGCGACA

       490        500        510        520        530        540
GGCAGCCATG AGCTGAGCAC ACACCCGGCC CGGCCACCAG GGCTGTATGC TCCAGGGCAC

       550        560        570        580        590        600
AGGCCTCCAT GCGCTCTTCT CTCTCTTTCC AGCCCCCGAC ATCAACCCTG CCTGGTACGC

       610        620        630        640        650        660
AGGCCGTGGG ATCCGGCCCG TGGGCCGCTT CGGCCGGCGA AGAGCTGCCC TGGGGGACGG

       670        680        690        700        710        720
ACCCAGGCCT GGCCCCCGGC GTGTGCCGGC CTGCTTCCGC CTGGAAGGCG GTGCTGAGCC

       730        740        750        760        770        780
CTCCCGAGCC CTCCCGGGGC GGCTGACGGC CCAGCTGGTC CAGGAATAA. ..........
```

FIG. 29

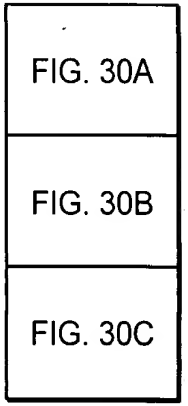


FIG. 30

```
                    10         20         30         40         50
genome      1 ATGAAGGCGG TGGGGGCCTG GCTCCTCTGC CTGCTGCTGC TGGGCCTGGC   50
cDNA        1 ATGAAGGCGG TGGGGGCCTG GCTCCTCTGC CTGCTGCTGC TGGGCCTGGC   50

                    60         70         80         90        100
genome     51 CCTGCAGGGG GCTGCCAGCA GAGCCCACCA GCACTCCATG GAGATCCGCA  100
cDNA       51 CCTGCAGGGG GCTGCCAGCA GAGCCCACCA GCACTCCATG GAGATCCGCA  100

                   110        120        130        140        150
genome    101 GTGAGTGTCT AGCCCCGCCC CTGCCCCCAG GGGTCACAGG GGGGGCCTGG  150
cDNA      101 ---------- ---------- ---------- ---------- ----------  150

                   160        170        180        190        200
genome    151 CCACTTCCTG GGCTGGGACA TCCTTGCTAA GCATCCTGGG GTTGGGGTTT  200
cDNA      151 ---------- ---------- ---------- ---------- ----------  200
```

FIG. 30A

```
                    210         220         230         240         250
genome    201 GGCCTCCTGT TCCCCAGACC CTTCCCCCAG GTGGCCCGGA CAGGTGCTCC  250
cDNA      201 ---------- ---------- ---------- ---------- ----------  250

                    260         270         280         290         300
genome    251 CAAGGGTCCC GGCCCAGCAC ACGGGGGAGG GTCACTCCTC ACCACACGGG  300
cDNA      251 ---------- ---------- ---------- ---------- ----------  300

                    310         320         330         340         350
genome    301 TGGCCTGGGG CTGAGTGCAC GTCACCCATG AGAACGGGGC TGTGAGGACA  350
cDNA      301 ---------- ---------- ---------- ---------- ----------  350

                    360         370         380         390         400
genome    351 GGAAAGGAAG GGGAGTGTGT CCTGGTGTGA GTCTGAAATC CTACTTCCCA  400
cDNA      351 ---------- ---------- ---------- ---------- ----------  400

                    410         420         430         440         450
genome    401 AAGCCACCCC AGCACCAGAA ATGGGCGGTC CGGGTGAACC TCCTGTGCGG  450
cDNA      401 ---------- ---------- ---------- ---------- ----------  450

                    460         470         480         490         500
genome    451 GTGGGTGGTC CTGGCATGGC CTGGGCGACA GGCAGCCATG AGCTGAGCAC  500
cDNA      451 ---------- ---------- ---------- ---------- ----------  500
```

FIG. 30B

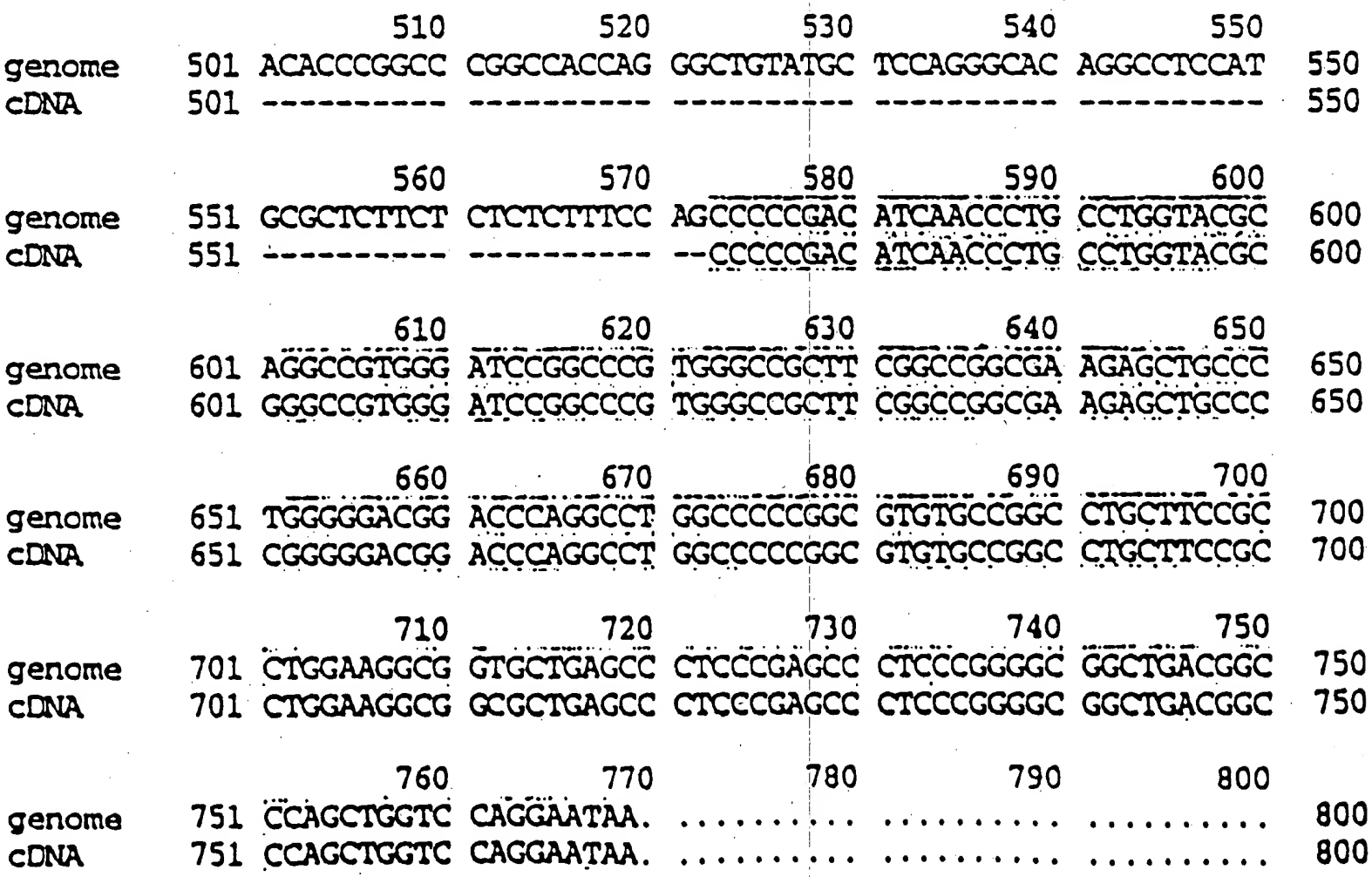

510 520 530 540 550
genome 501 ACACCCGGCC CGGCCACCAG GGCTGTATGC TCCAGGGCAC AGGCCTCCAT 550
cDNA 501 ---------- ---------- ---------- ---------- ---------- 550
560 570 580 590 600
genome 551 GCGCTCTTCT CTCTCTTTCC AGCCCCCGAC ATCAACCCTG CCTGGTACGC 600
cDNA 551 ---------- ---------- --CCCCCGAC ATCAACCCTG CCTGGTACGC 600
610 620 630 640 650
genome 601 AGGCCGTGGG ATCCGGCCCG TGGGCCGCTT CGGCCGGCGA AGAGCTGCCC 650
cDNA 601 GGGCCGTGGG ATCCGGCCCG TGGGCCGCTT CGGCCGGCGA AGAGCTGCCC 650
660 670 680 690 700
genome 651 TGGGGGACGG ACCCAGGCCT GGCCCCCGGC GTGTGCCGGC CTGCTTCCGC 700
cDNA 651 CGGGGGACGG ACCCAGGCCT GGCCCCCGGC GTGTGCCGGC CTGCTTCCGC 700
710 720 730 740 750
genome 701 CTGGAAGGCG GTGCTGAGCC CTCCCGAGCC CTCCCGGGGC GGCTGACGGC 750
cDNA 701 CTGGAAGGCG GCGCTGAGCC CTCCCGAGCC CTCCCGGGGC GGCTGACGGC 750
760 770 780 790 800
genome 751 CCAGCTGGTC CAGGAATAA. 800
cDNA 751 CCAGCTGGTC CAGGAATAA. 800

FIG. 30C

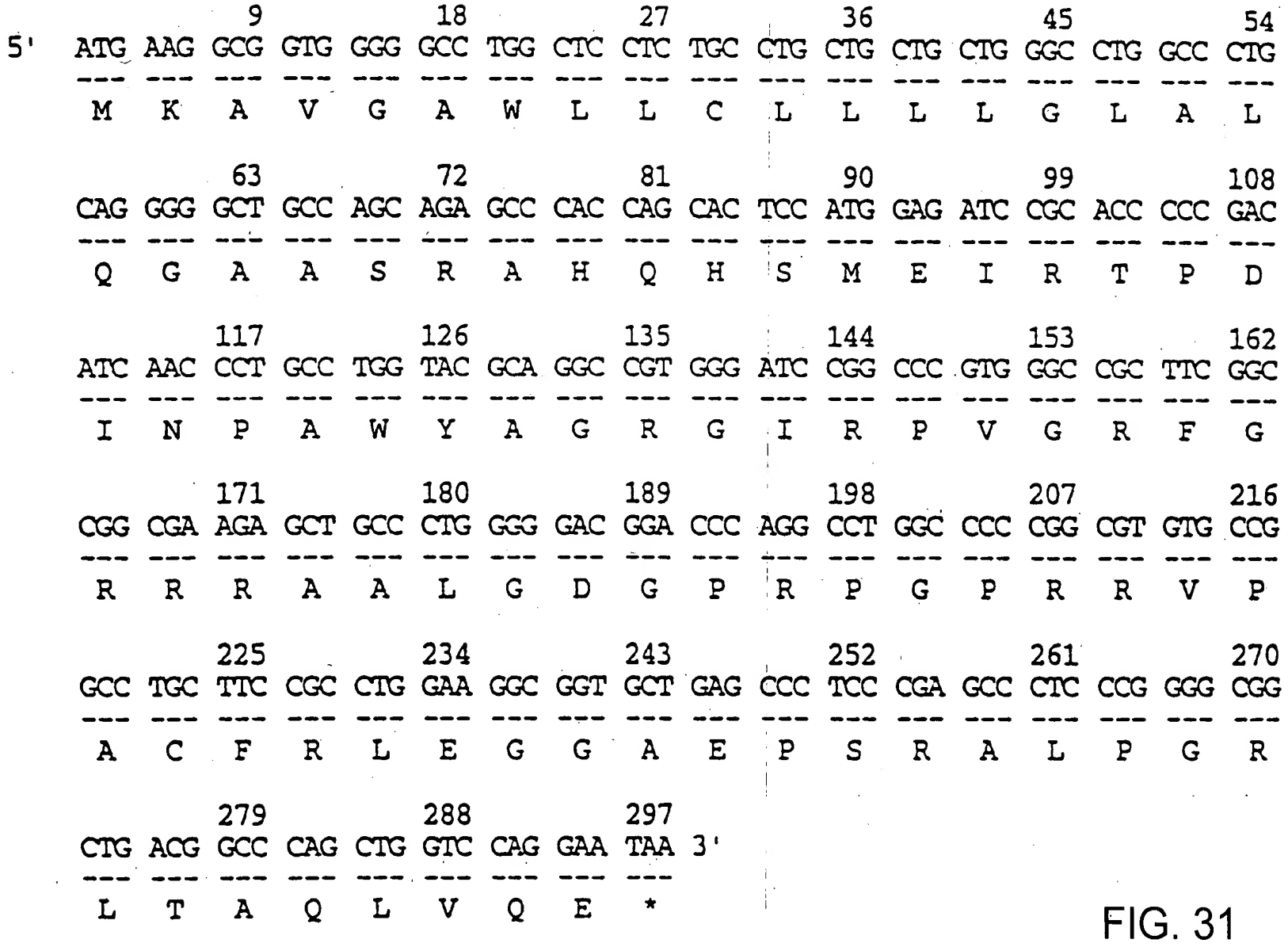

5'
9 18 27 36 45 54
ATG AAG GCG GTG GGG GCC TGG CTC CTC TGC CTG CTG CTG CTG GGC CTG GCC CTG
M K A V G A W L L C L L L L G L A L
63 72 81 90 99 108
CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC
Q G A A S R A H Q H S M E I R T P D
117 126 135 144 153 162
ATC AAC CCT GCC TGG TAC GCA GGC CGT GGG ATC CGG CCC GTG GGC CGC TTC GGC
I N P A W Y A G R G I R P V G R F G
171 180 189 198 207 216
CGG CGA AGA GCT GCC CTG GGG GAC GGA CCC AGG CCT GGC CCC CGG CGT GTG CCG
R R R A A L G D G P R P G P R R V P
225 234 243 252 261 270
GCC TGC TTC CGC CTG GAA GGC GGT GCT GAG CCC TCC CGA GCC CTC CCG GGG CGG
A C F R L E G G A E P S R A L P G R
279 288 297
CTG ACG GCC CAG CTG GTC CAG GAA TAA 3'
L T A Q L V Q E *

FIG. 31

```
  1  GGCATCATCCAGGAAGACGGAGCATGGCCCTGAAGACGTGGCTTCTGTGCTTGCTGCTG     59
  1                                MetAlaLeuLysThrTrpLeuLeuCysLeuLeuLeu     12

 60 CTAAGCTTGGTCCTCCCAGGGGCTTCCAGCCGAGCCCACCAGCACTCCATGGAGACAAGA    119
 13 LeuSerLeuValLeuProGlyAlaSerSerArgAlaHisGlnHisSerMetGluThrArg     32

120 ACCCCTGATATCAATCCTGCCTGGTACACGGGCCGCGGGATCAGGCCTGTGGGCCGCTTC    179
 33 ThrProAspIleAsnProAlaTrpTyrThrGlyArgGlyIleArgProValGlyArgPhe     52

180 GGCAGGAGAAGGGCAACCCCGAGGGATGTCACTGGACTTGGCCAACTCAGCTGCCTCCCA    239
 53 GlyArgArgArgAlaThrProArgAspValThrGlyLeuGlyGlnLeuSerCysLeuPro     72

240 CTGGATGGACGCACCAAGTTCTCTCAGCGTGGATAACACCCCAGCTCGAGAAGACAGTGC    299
 73 LeuAspGlyArgThrLysPheSerGlnArgGly***                           83

300 TGCTGAGCCCAAGCCCACACTCCCTGTCCCCTGCAGACCCTCCTCTACCCTCCCTCTCCT    359
 83                                                                83

360 CTGCT                                                          364
 83                                                                83
```

FIG. 32

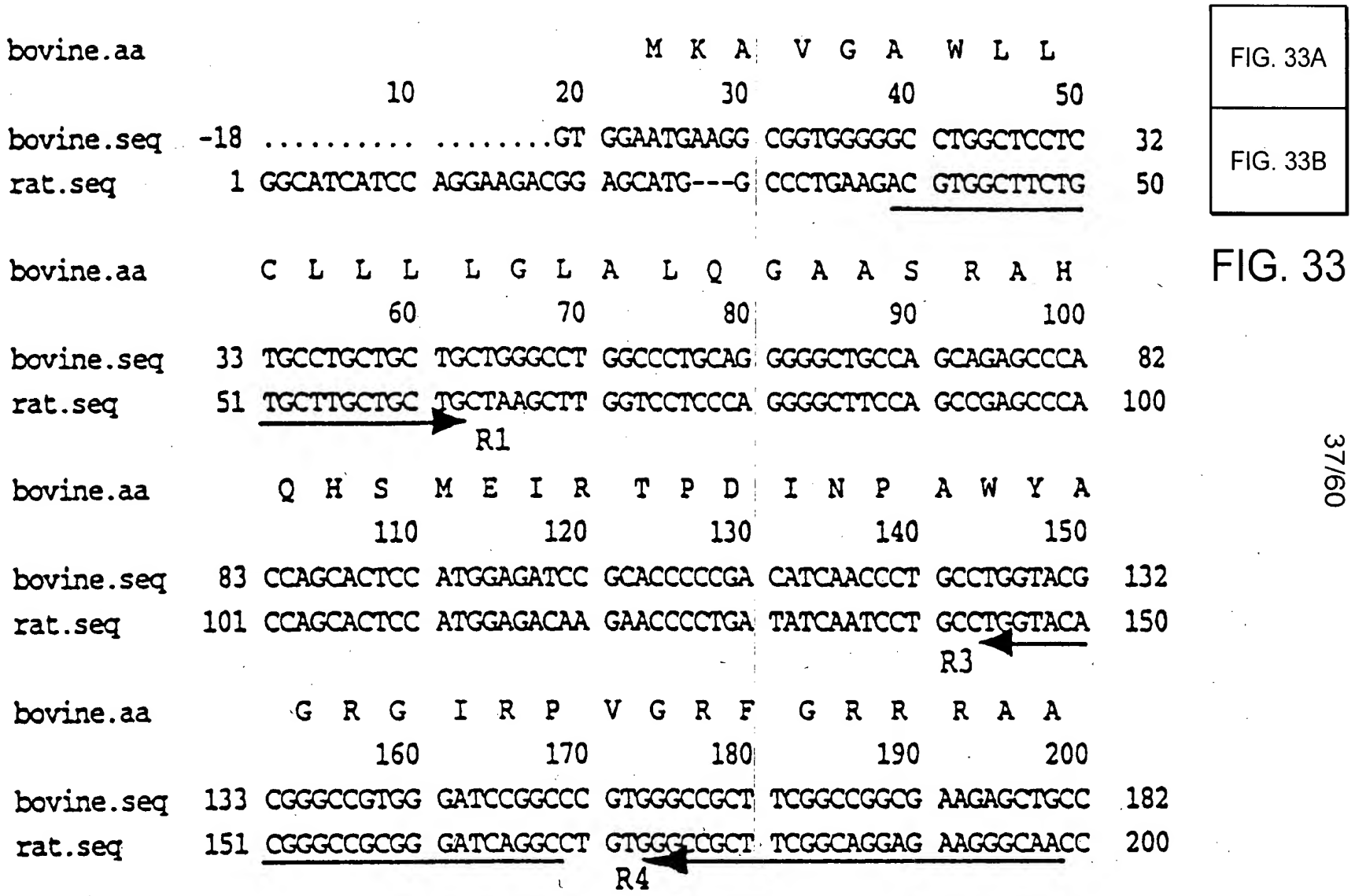


FIG. 33A

FIG. 33B

FIG. 33

FIG. 33A

```
bovine.aa          P  G  D  G   P  R  P   G  P  R  R  V  P  A   C  F  R
                             210         220         230         240         250
bovine.seq    183 CCGGGGGACG GACCCAGGCC TGGCCCCCGG CGTGTGCCGG CCTGCTTCCG  232
rat.seq       201 CCGAGGGATG TCACTGGACT TGGC------ ---CAACTCA GCTGCCTCCC  250

bovine.aa          L  E  G   G  A  E  P   S  R  A   L  P  G  R   L  T  A
                             260         270         280         290         300
bovine.seq    233 CCTGGAAGGC GGCGCTGAGC CCTCCCGAGC CCTCCCGGGG CGGCTGACGG  282
rat.seq       251 ACTGGATGGA CGCACCAAGT TCTCTCAGCG TGGATAACAC CCCAGCTCGA  300

bovine.aa          Q  L  V   Q  E  *
                             310         320         330         340         350
bovine.seq    283 CCCAGCTGGT CCAGGAATAA CAGCGGGAGC CTGCCCCCCA CCCCTCCTCC  332
rat.seq       301 GAAGACAGTG CTGCTGAGCC CAAGCCCACA CTCCCTGTCC CCTGCAGACC  350

                             360         370         380         390         400
bovine.seq    333 TCCACCAGCC ACCTTCCCTC CAGTCCTAAT AAAAGCAGCT GGCTTGTT..  382
rat.seq       351 CTCCTCTACC CTCCCTCTCC TCTGCT.... .......... ..........  400
```

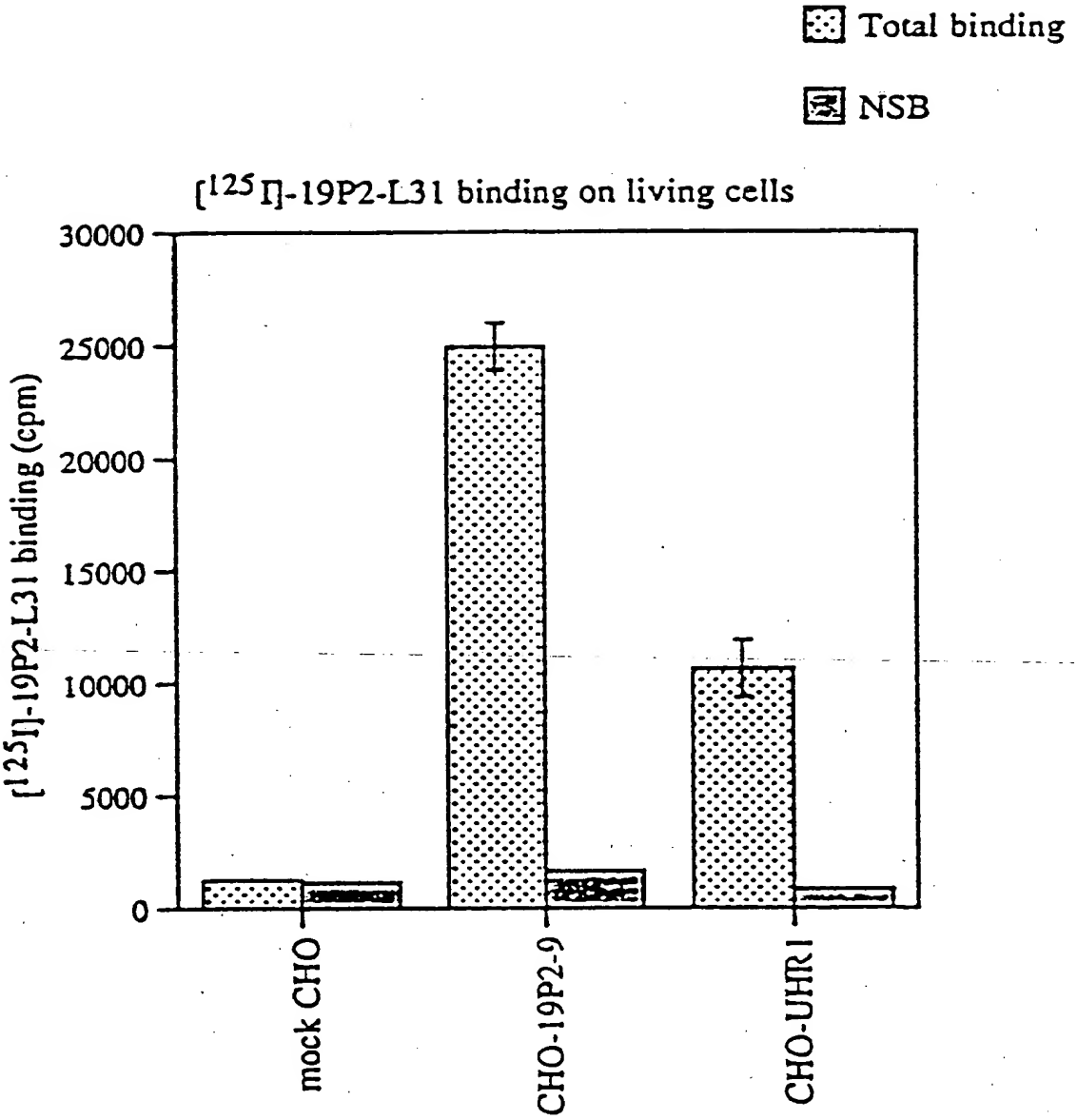
FIG. 33B

```
  1  GGCCTCCTCGGAGGAGCCAAGGGATGAAGGTGCTGAGGGCCTGGCTCCTGTGCCTGCTG    59
  1                                MetLysValLeuArgAlaTrpLeuLeuCysLeuLeu    12

 60 ATGCTGGGCCTGGCCCTGCGGGGAGCTGCAAGTCGTACCCATCGGCACTCCATGGAGATC    119
 13 MetLeuGlyLeuAlaLeuArgGlyAlaAlaSerArgThrHisArgHisSerMetGluIle    32

120 CGCACCCCTGACATCAATCCTGCCTGGTACGCCAGTCGCGGGATCAGGCCTGTGGGCCGC    179
 33 ArgThrProAspIleAsnProAlaTrpTyrAlaSerArgGlyIleArgProValGlyArg    52

180 TTCGGTCGGAGGAGGGCAACCCTGGGGGACGTCCCCAAGCCTGGCCTGCGACCCCGGCTG    239
 53 PheGlyArgArgArgAlaThrLeuGlyAspValProLysProGlyLeuArgProArgLeu    72

240 ACCTGCTTCCCCCTGGAAGGCGGTGCTATGTCGTCCCAGGATGGCTGACAGCCAGCTTGT    299
 73 ThrCysPheProLeuGluGlyGlyAlaMetSerSerGlnAspGly***               87

300 CAAGAAACTCACTCTGGAGCCTCCCCCACCCCACCCTCTCCTCTCCTTCGGGCTCCTTTC    359
 87                                                                 87

360 CC                                                             361
 87                                                                 87
```

FIG. 34

```
                      10         20         30         40         50
bovine.aa      1 MKAVGAWLLC LLLLGLALQG AASRAHQHSM EIRTPDINPA WYAGRGIRPV      50
rat.aa         1 M-ALKTWLLC LLLLSLVLPG ASSRAHQHSM ETRTPDINPA WYTGRGIRPV      50
human.aa       1 MKVLRAWLLC LLMLGLALRG AASRTHRHSM EIRTPDINPA WYASRGIRPV      50

                      60         70         80         90        100
bovine.aa     51 GRFGRRRAAP GDGPRPGPRR VPACFRLEGG AEPSRALPGR LTAQLVQE*.     100
rat.aa        51 GRFGRRRATP RDVTGLG--- QLSCLPLDGR TKFSQRG*.. ..........     100
human.aa      51 GRFGRRRATL GDVPKPGLRP RLTCFPLEGG AMSSQDG*.. ..........     100
```

FIG. 35



cells; 0.5 x 10^7 cells/ml
[^{125} I]-19P2-L31; 200pM(avg.63857.3cpm)
NSB; 200nM(x 1,000)
reaction; RT, 2.5hr
in HBSS + 0.05% BSA + 0.05% CHAPS
in 100 µl

FIG. 36

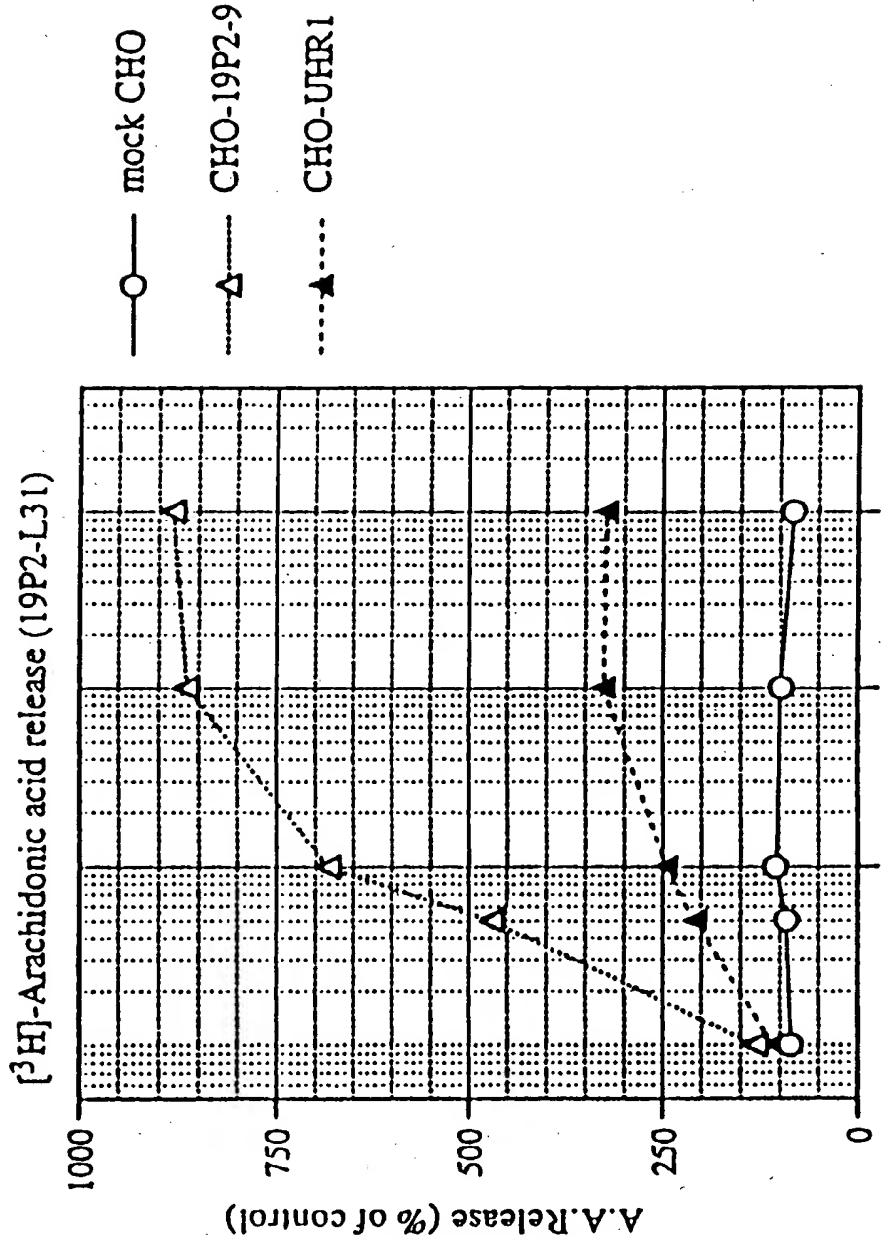

mock CHO
CHO-19P2-9
CHO-UHR1
[3H]-Arachidonic acid release (19P2-L31)
A.A.Release (% of control)
1000
750
500
250
0
1
10
100
19P2-L31 (x 10-9M)

FIG. 37

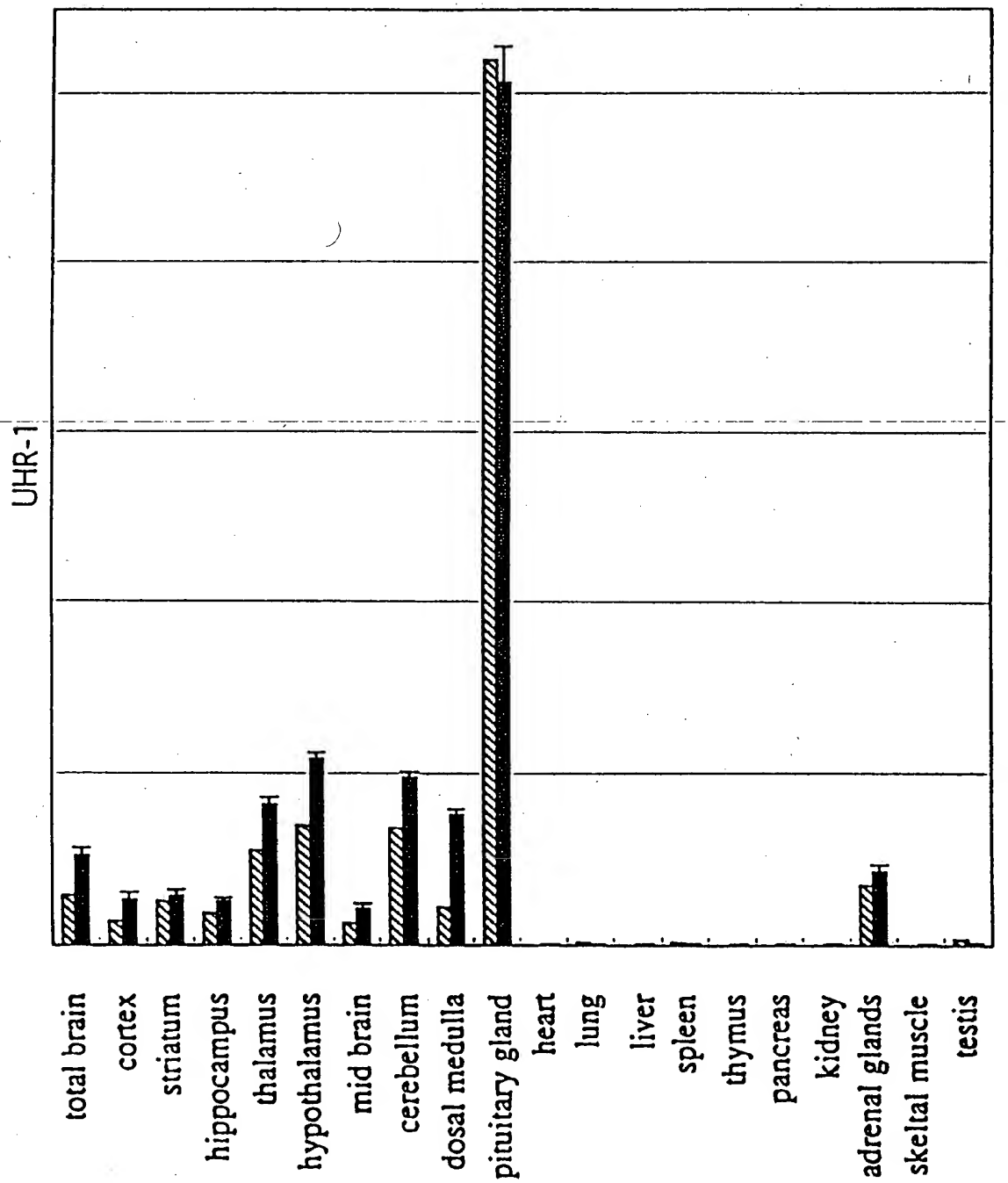

UHR-1
total brain
cortex
striatum
hippocampus
thalamus
hypothalamus
mid brain
cerebellum
dosal medulla
pituitary gland
heart
lung
liver
spleen
thymus
pancreas
kidney
adrenal glands
skeltal muscle
testis
0
2
4
6
8
10
receptor±S.E.M.(pgx10-3/4ng polyA+RNA)
receptor/G3PDH(x2.5x10-2)

FIG. 38

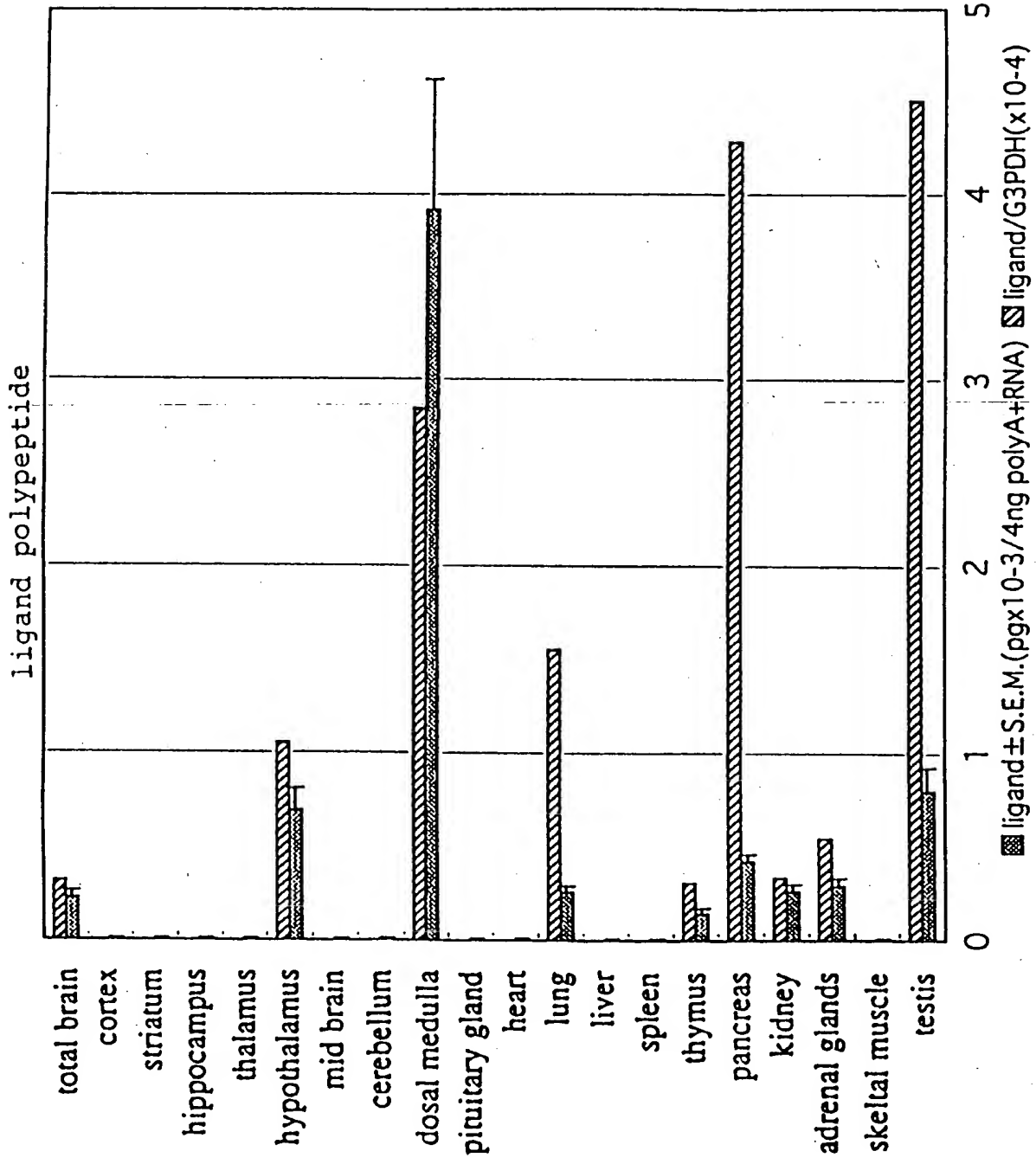

ligand polypeptide
total brain
cortex
striatum
hippocampus
thalamus
hypothalamus
mid brain
cerebellum
dosal medulla
pituitary gland
heart
lung
liver
spleen
thymus
pancreas
kidney
adrenal glands
skeltal muscle
testis
0
1
2
3
4
5
ligand±S.E.M.(pgx10-3/4ng polyA+RNA)
ligand/G3PDH(x10-4)

FIG. 39

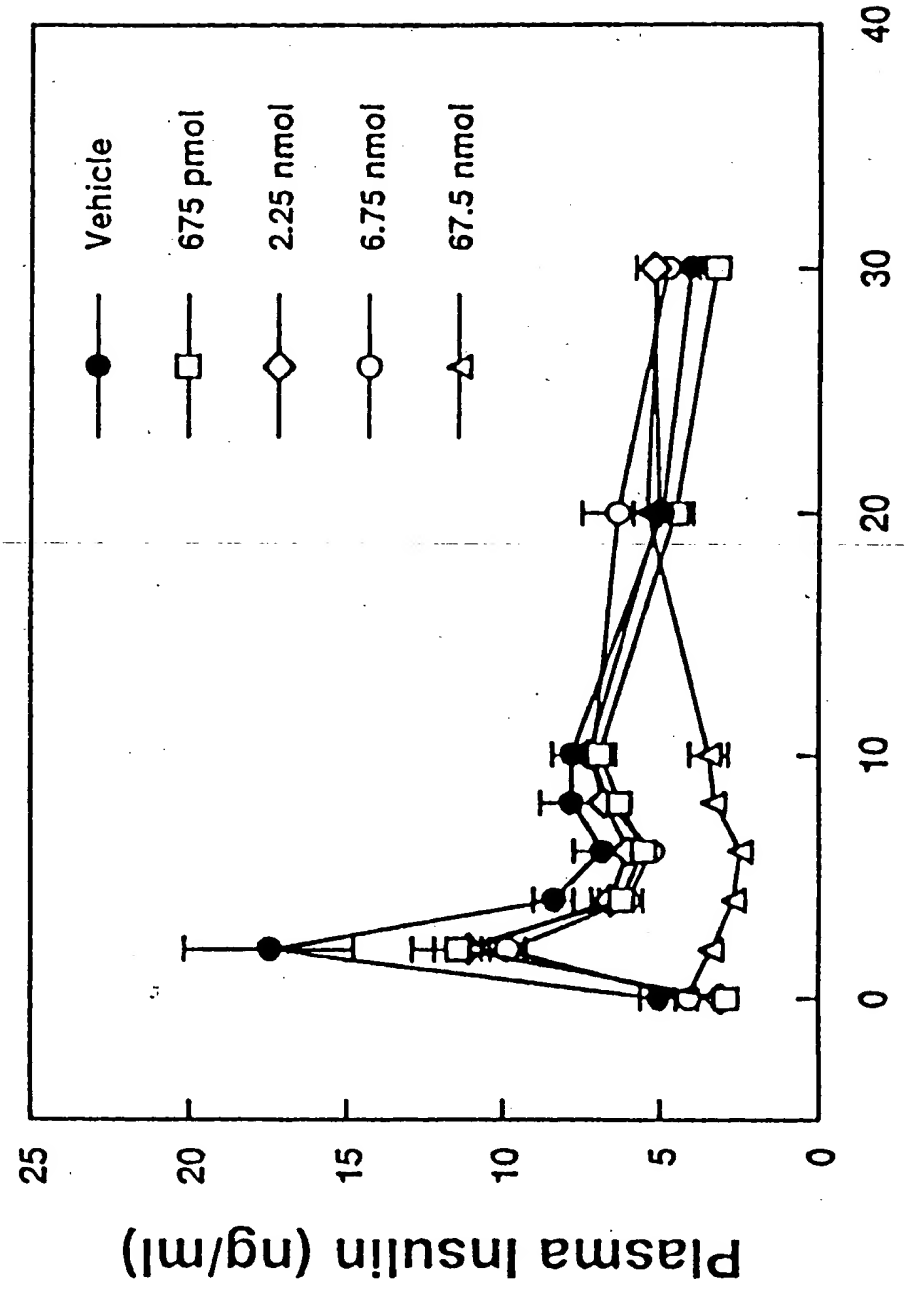

Plasma Insulin (ng/ml)
25
20
15
10
5
0
Time (min)
0
10
20
30
40
Vehicle
675 pmol
2.25 nmol
6.75 nmol
67.5 nmol

FIG. 40

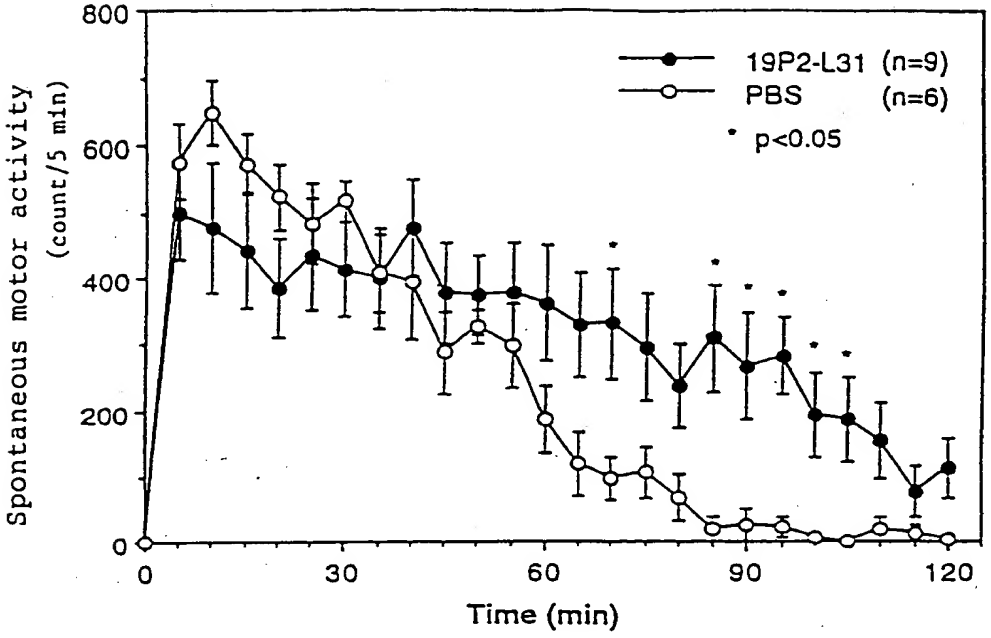


FIG. 41A

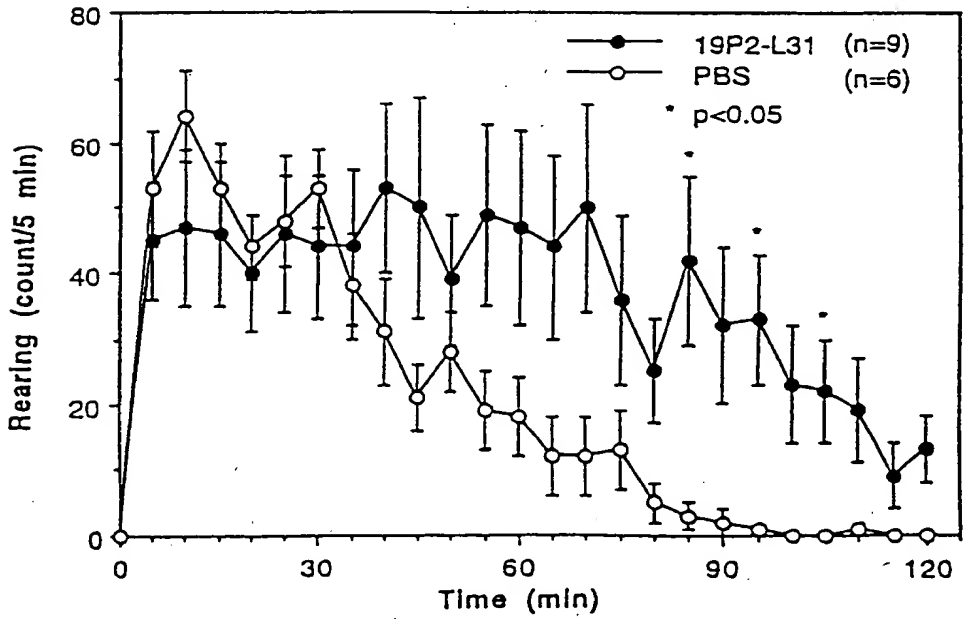


FIG. 41B

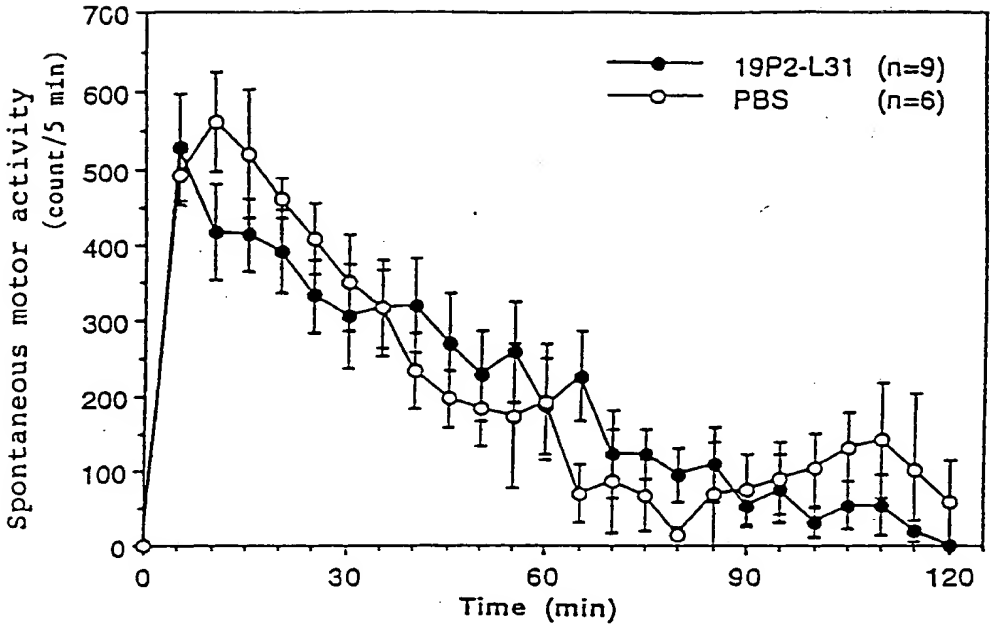


FIG. 42A

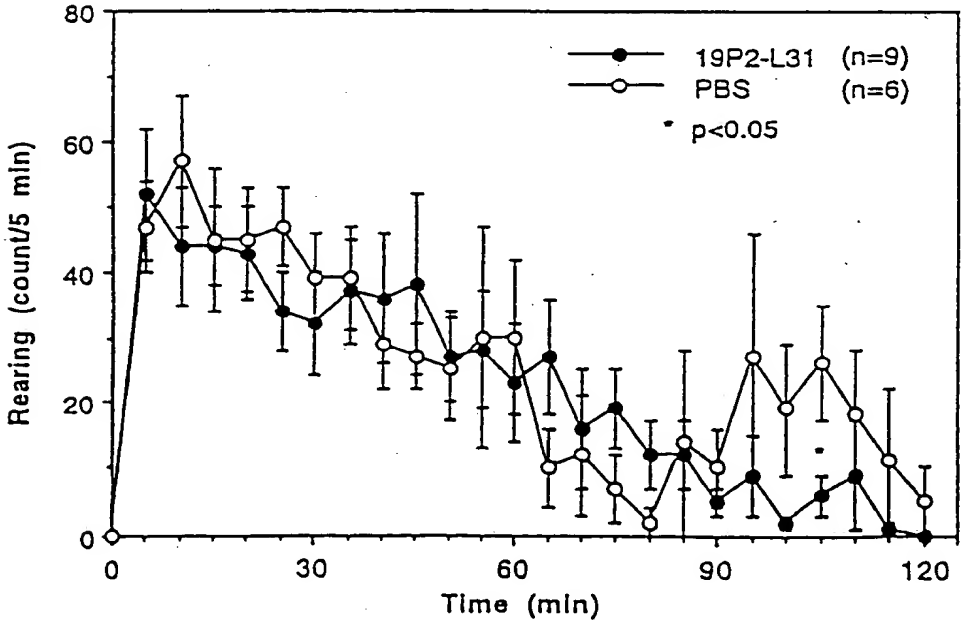


FIG. 42B

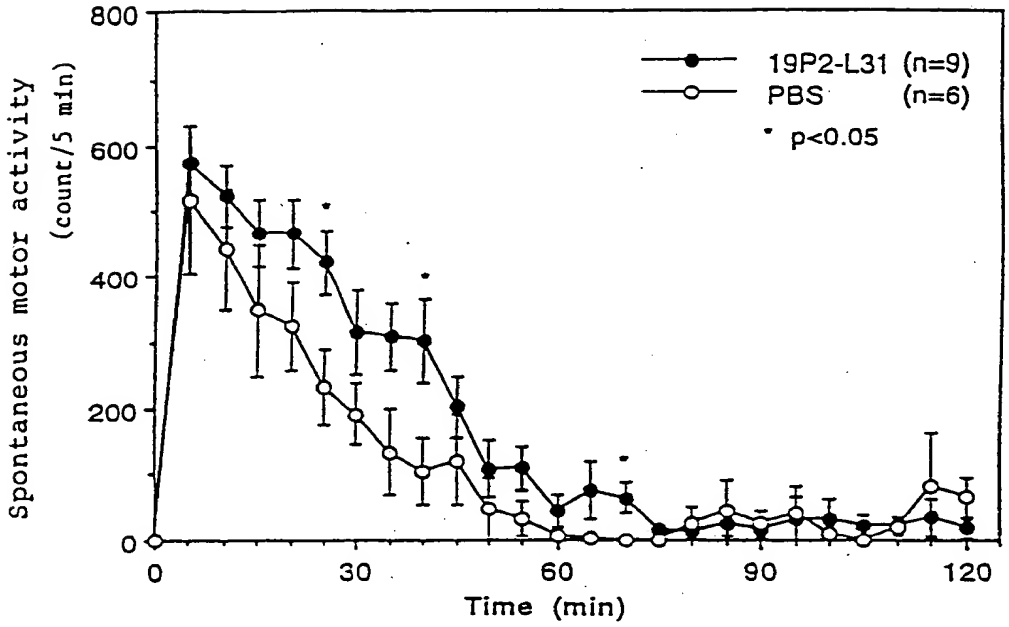


FIG. 43A

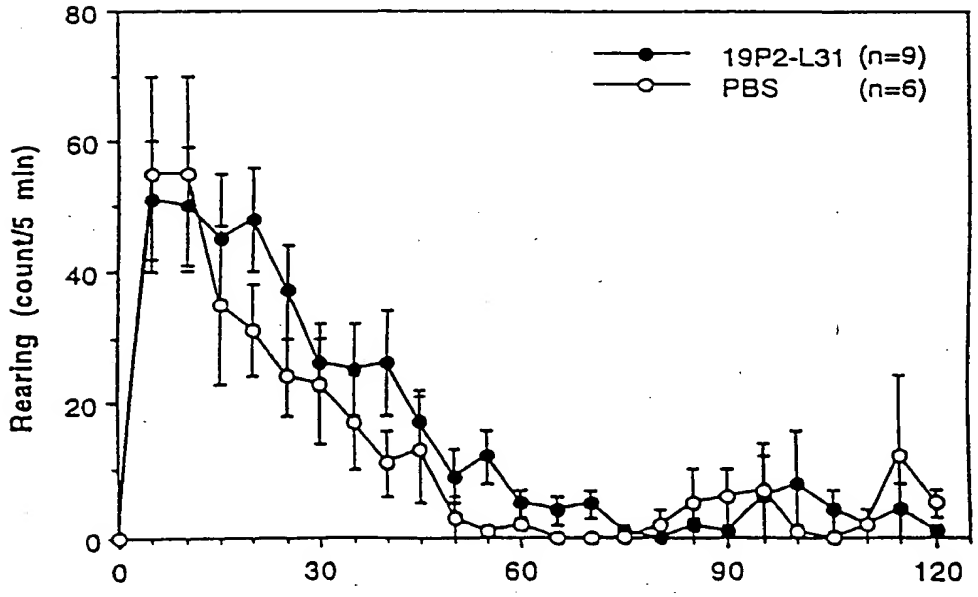


FIG. 43B

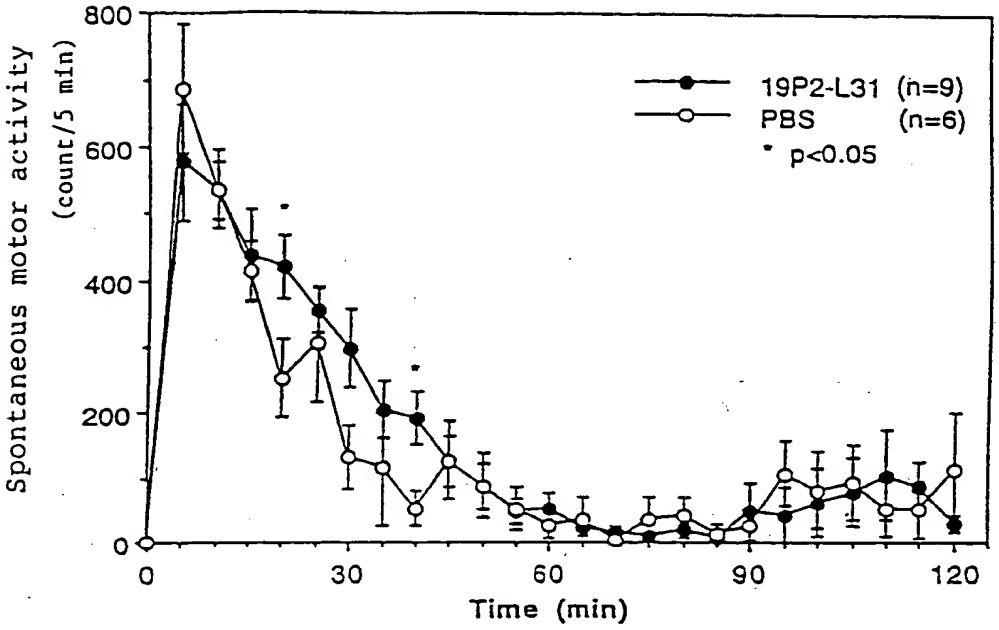


FIG. 44A

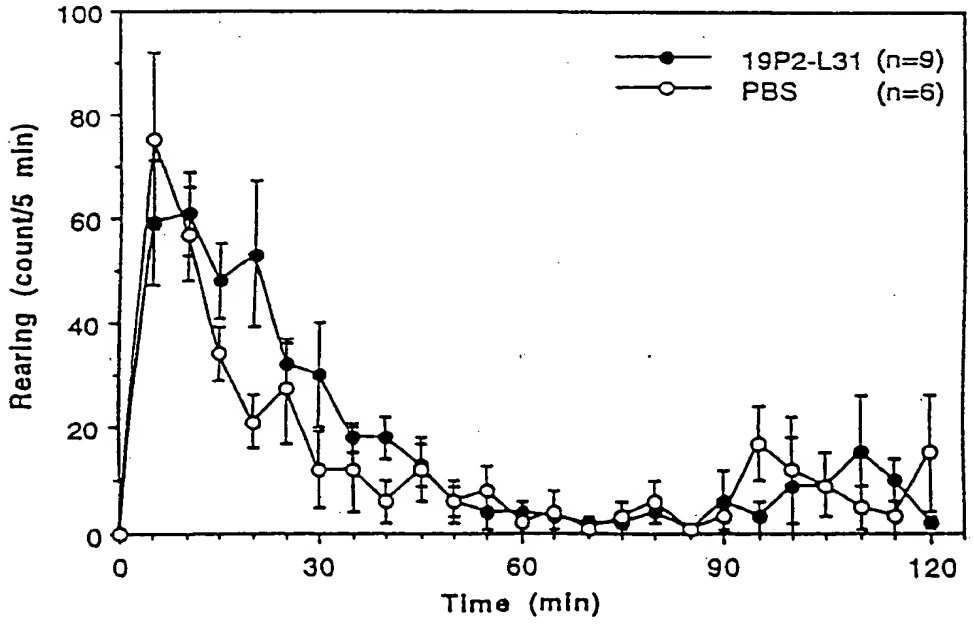


FIG. 44B

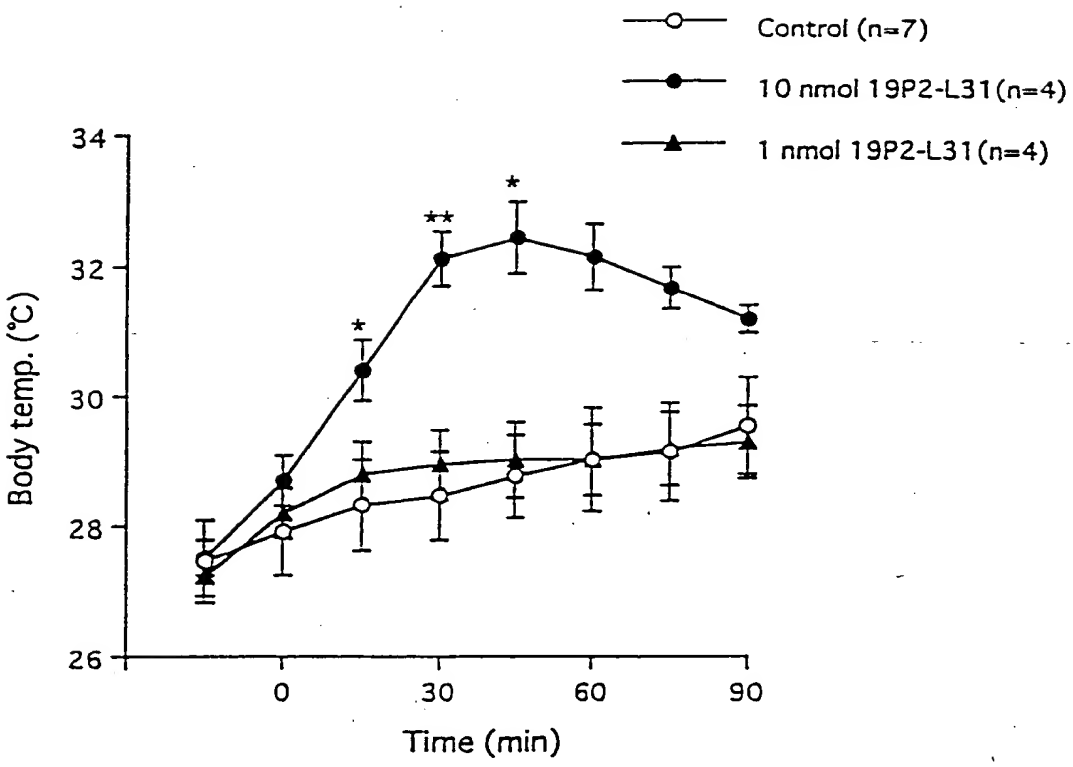

Control (n=7)
10 nmol 19P2-L31(n=4)
1 nmol 19P2-L31(n=4)
Body temp. (°C)
34
32
30
28
26
0
30
60
90
Time (min)
*
**
*

FIG. 45

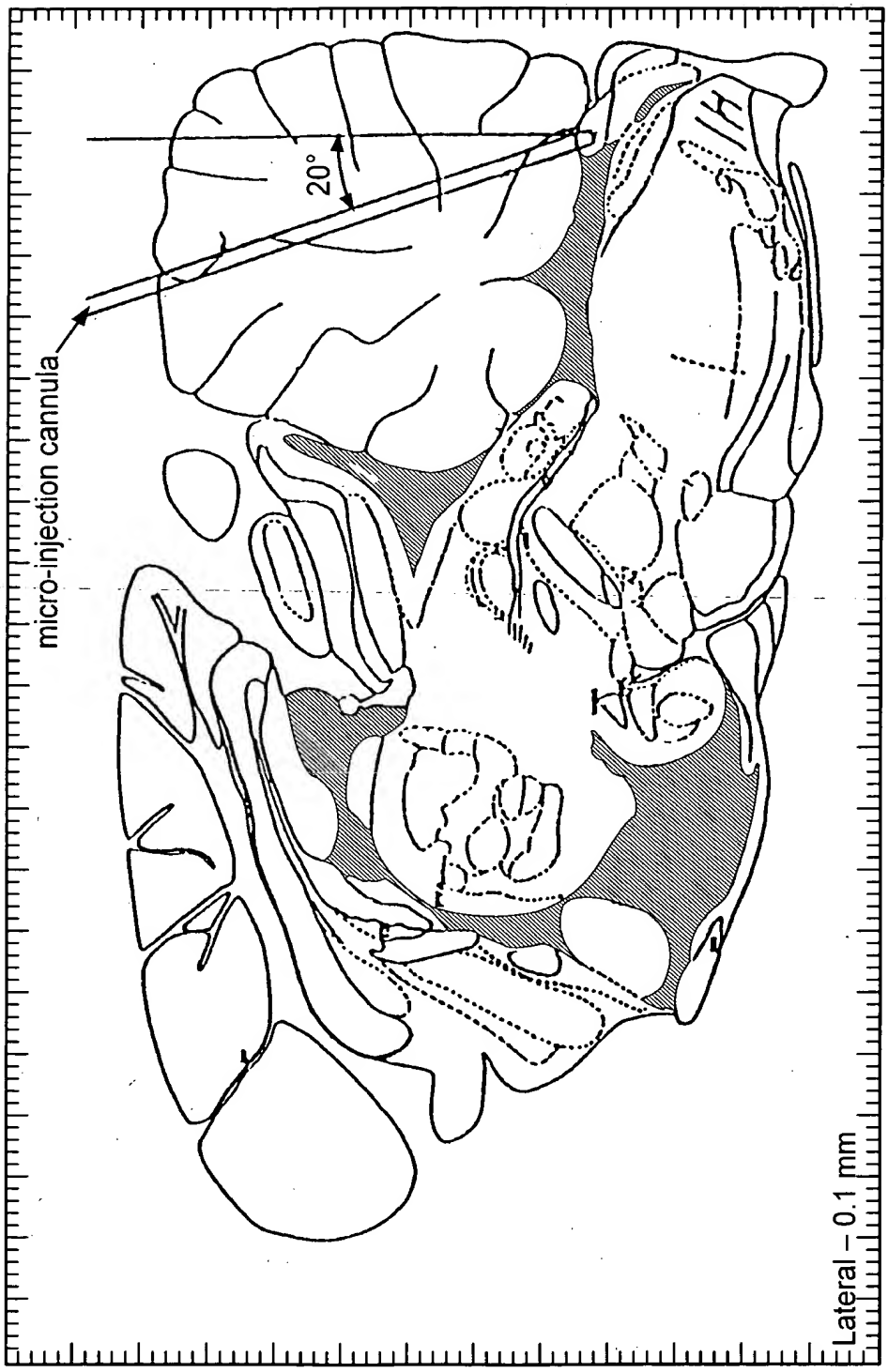


FIG. 46

direct blood pressure

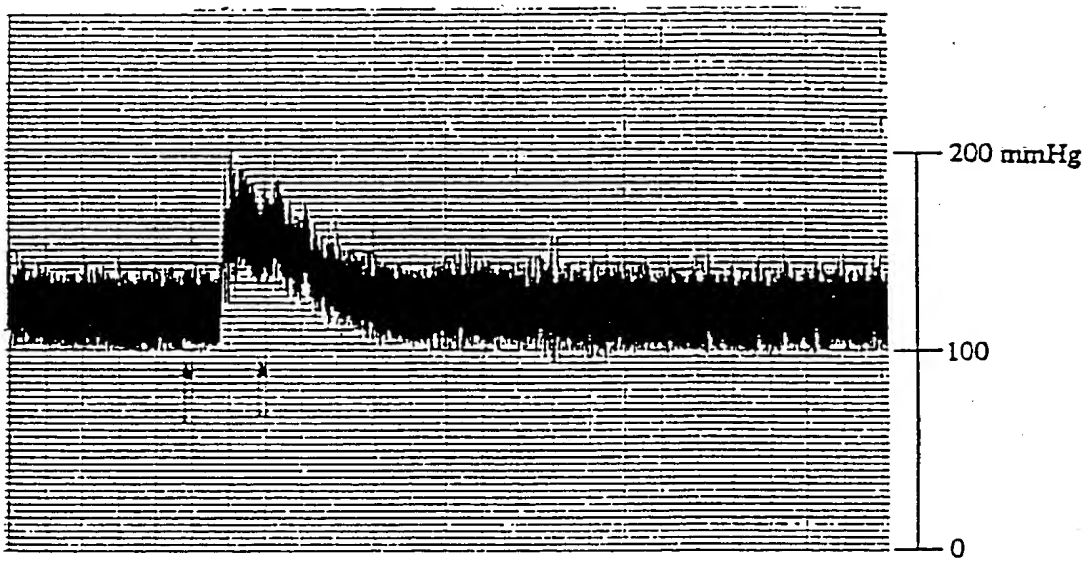


FIG. 47A

mean blood pressure

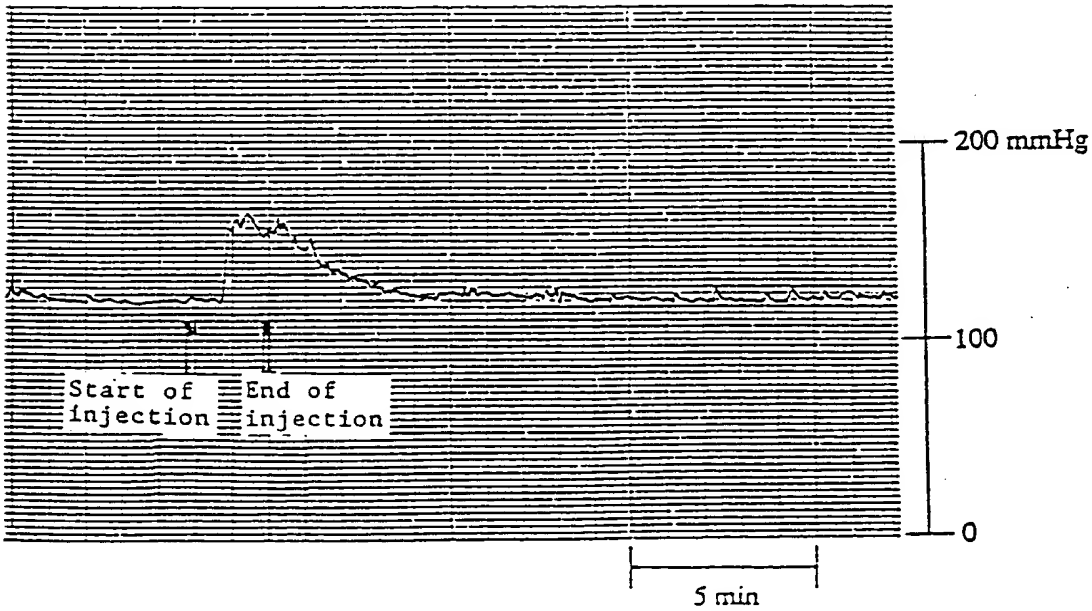


FIG. 47B

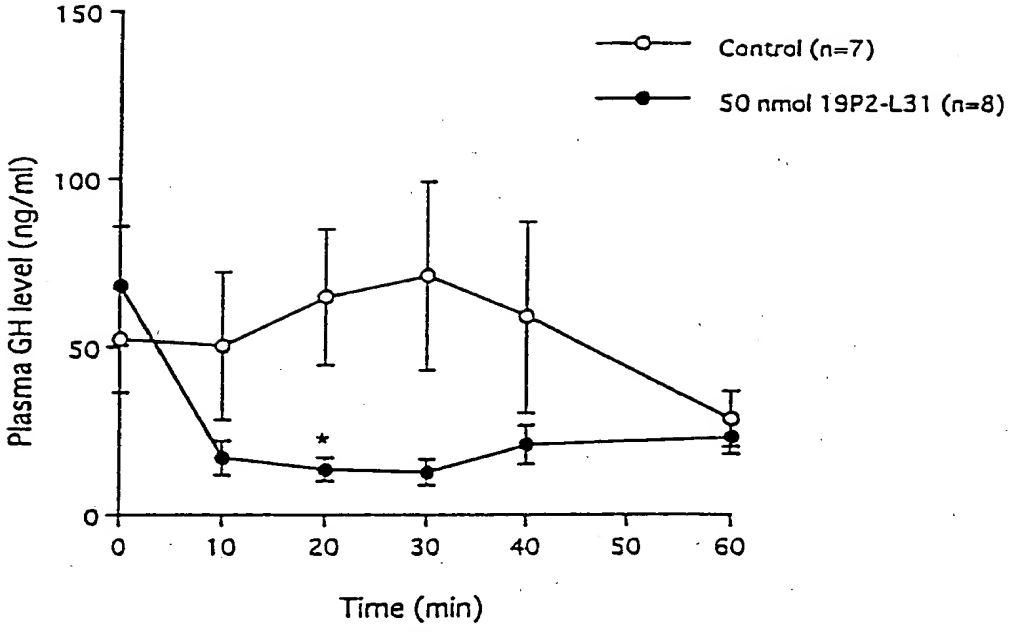

150
100
50
0
Plasma GH level (ng/ml)
0
10
20
30
40
50
60
Time (min)
Control (n=7)
50 nmol 19P2-L31 (n=8)
*

FIG. 48

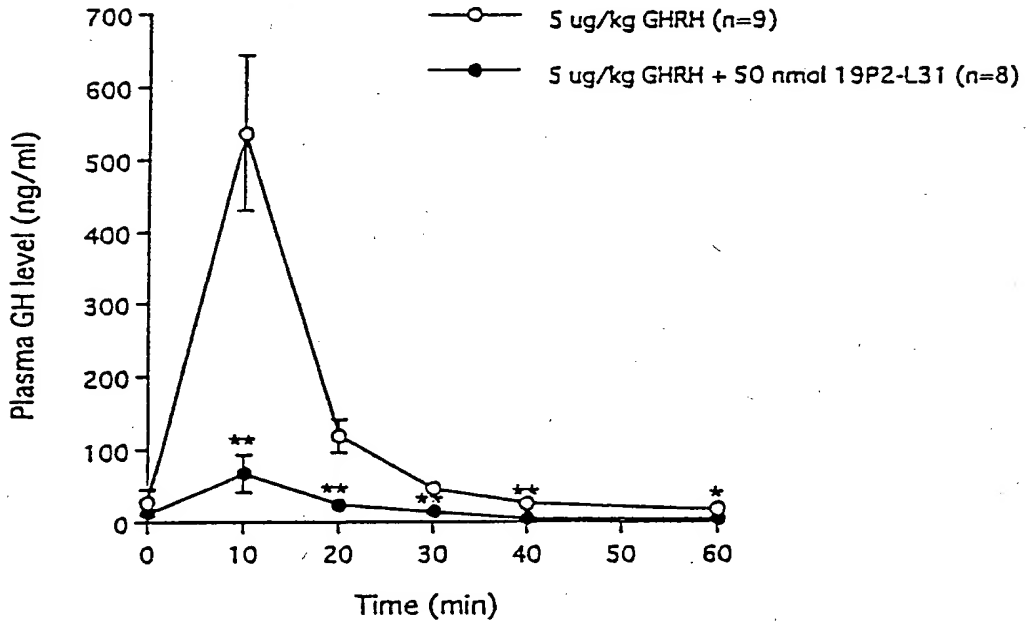

700
600
500
400
300
200
100
0
Plasma GH level (ng/ml)
0
10
20
30
40
50
60
Time (min)
5 ug/kg GHRH (n=9)
5 ug/kg GHRH + 50 nmol 19P2-L31 (n=8)
**
**
**
**
*

FIG. 49

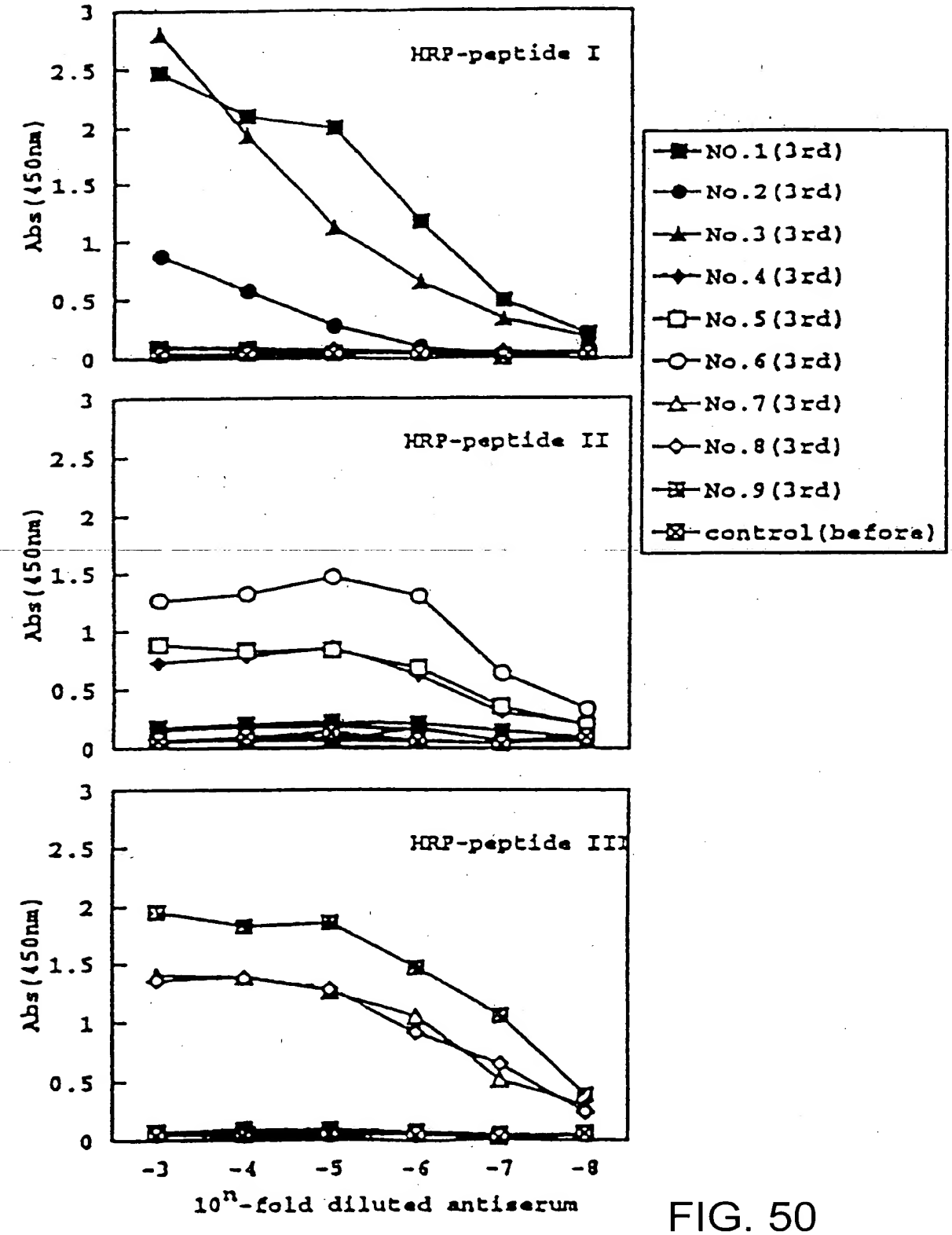

HRP-peptide I
HRP-peptide II
HRP-peptide III
Abs(450nm)
3
2.5
2
1.5
1
0.5
0
-3
-4
-5
-6
-7
-8
10n-fold diluted antiserum
No.1(3rd)
No.2(3rd)
No.3(3rd)
No.4(3rd)
No.5(3rd)
No.6(3rd)
No.7(3rd)
No.8(3rd)
No.9(3rd)
control(before)

FIG. 50

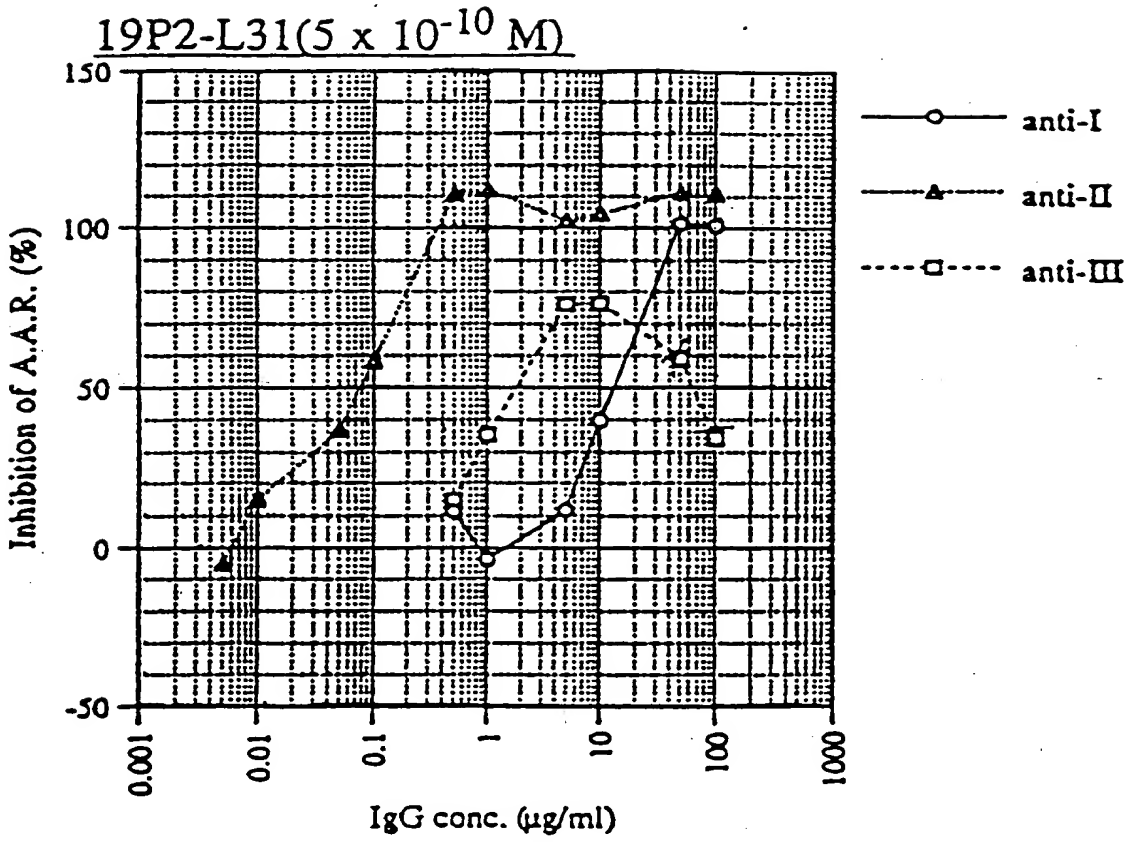

19P2-L31(5 x 10-10 M)
150
100
50
0
-50
Inhibition of A.A.R. (%)
0.001
0.01
0.1
1
10
100
1000
IgG conc. (μg/ml)
anti-I
anti-II
anti-III

FIG. 51

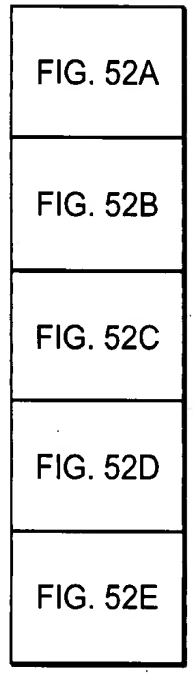


FIG. 52

FIG. 52A

```
                9          18          27          36          45          54
5'  ATG ACC TCA CTG CCC CCT GGA ACC ACT GGG GAC CCC GAT TTG TTT TCT GGG CCG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Thr Ser Leu Pro Pro Gly Thr Thr Gly Asp Pro Asp Leu Phe Ser Gly Pro

               63          72          81          90          89         108
    TCG CCA GCC GGC TCC ACT CCA GCC AAC CAG AGT GCA GAG GCT TCA GAG AGC AAT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Pro Ala Gly Ser Thr Pro Ala Asn Gln Ser Ala Glu Ala Ser Glu Ser Asn
```

```
        117         126         135         144         153         162
GTG TCT GCG ACG GTT CCC AGA GCT GCA GCA GTC ACG CCG TTC CAG AGC CTG CAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Ser Ala Thr Val Pro Arg Ala Ala Ala Val Thr Pro Phe Gln Ser Leu Gln

        171         180         189         198         207         216
CTA GTG CAC CAG CTG AAG GCA CTG ATC GTG ATG CTG TAC AGC ATC GTG GTG GTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Val His Gln Leu Lys Ala Leu Ile Val Met Leu Tyr Ser Ile Val Val Val

        225         234         243         252         261         270
GTG GGT CTG GTG GGC AAC TGC CTT CTT GTG CTG GTG ATC GCG CGC GTG CGC CGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Gly Leu Val Gly Asn Cys Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg

        279         288         297         306         315         324
CTG CAC AAC GTG ACC AAC TTC CTC ATC GGC AAC CTG GCC TTG TCC GAT GTG CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu

        333         342         351         360         369         378
ATG TGT GCC GCC TGT GTG CCT CTC ACG CTG GCC TAC GCC TTT GAA CCT CGT GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Met Cys Ala Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly
```

FIG. 52B

```
         387          396          405          414          423          432
TGG GTG TTC GGT GGA GGC CTG TGC CAC CTT GTT TTC TTC CTG CAG CCG GTC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr

         441          450          459          468          477          486
GTC TAC GTA TCG GTG TTC ACA CTC ACC ACA ATC GCT GTG GAC CGC TAT GTG GTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val

         495          504          513          522          531          540
CTG GTG CAC CCG CTA CGT CGG CGC ATT TCA CTG AAG CTC AGC GCC TAC GCT GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Lys Leu Ser Ala Tyr Ala Val

         549          558          567          576          585          594
CTG GGC ATC TGG GCT CTA TCT GCA GTG CTG GCG CTG CCG GCC GCG GTG CAC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr

         603          612          621          630          639          648
TAC CAT GTA GAG CTC AAG CCC CAC GAC GTG CGC CTC TGC GAG GAG TTC TGG GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Tyr His Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly
```

FIG. 52C

```
         657          666          675          684          693          702
TCG CAG GAG CGC CAG CGA CAG ATC TAT GCC TGG GGG CTG CTG CTG GGC ACC TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ser Gln Glu Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr

         711          720          729          738          747          756
TTG CTC CCC CTG CTG GCC ATT CTC CTG TCT TAC GTC CGG GTG TCG GTG AAG TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu

         765          774          783          792          801          810
CGG AAC CGC GTG GTG CCT GGC AGC GTG ACC CAG AGC CAG GCT GAC TGG GAC CGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg

         819          828          837          846          855          864
GCG CGT CGC CGT CGC ACT TTC TGC CTG CTG GTG GTG GTG GTG GTC GTG TTC GCG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala

         873          882          891          900          909          918
GTC TGC TGG CTG CCT CTG CAC ATT TTC AAC CTG CTG CGG GAC CTG GAC CCG CGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Cys Trp Leu Pro Leu His Ile Phe Asn Leu Leu Arg Asp Leu Asp Pro Arg
```

FIG. 52D

```
        927         936         945         954         963         972
GCC ATC GAC CCC TAC GCC TTC GGG CTG GTG CAG CTC CTC TGC CAC TGG CTT GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys His Trp Leu Ala

        981         990         999        1008        1017        1026
ATG AGC TCC GCC TGC TAC AAC CCC TTC ATC TAT GCG TCG CTG CAC GAC AGC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Ser Leu His Asp Ser Phe

       1035        1044        1053        1062        1071        1080
CGA GAG GAG CTA CGC AAG ATG CTT CTG TCT TGG CCC CGC AAG ATC GTG CCT CAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Arg Glu Glu Leu Arg Lys Met Leu Leu Ser Trp Pro Arg Lys Ile Val Pro His

      1089        1098        1107        1116
GGC CAG AAT ATG ACC GTC AGT GTG GTC ATC TGA TGA
--- --- --- --- --- --- --- --- --- --- --- --- 1'
Gly Gln Asn Met Thr Val Ser Val Val Ile --- ---
```


FIG. 52E